

GenCore version 5.1.6  
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## OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 19, 2003, 15:30:30 ; Search time 124 Seconds

(Without alignments)  
2694.573 Million cell updates/sec

Title: US-09-494-297-2

Perfect score: 3945

Sequence: 1 MKRFRPNKLTNTQRYLS.....IAGISLGWGTHTIRKHD 757

## Scoring table:

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
Delop 6.0	Delext 7.0	

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

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-DB=Issued\_Patents\_NA -QEXT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

## Database :

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5: /cgn2\_6/ptodata/1/ina/PCRTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfilltest.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	182	4.6	2187	4	US-09-107-532A-864
2	178	4.5	2694	3	US-08-867-941-2
3	178	4.5	2694	2	US-09-074-658-2
4	178	4.5	7650	3	US-08-867-941-1
5	178	4.5	7650	2	US-09-074-658-1
6	176	4.5	2718	3	US-09-074-658-69
7	161	4.1	4249	4	US-09-071-035-403
8	161	4.1	4359	4	US-09-071-035-401
9	152	3.9	5547	4	US-08-851-567B-48
10	152	3.9	7551	4	US-08-851-567B-46
11	150	3.8	3531	2	US-08-714-402-1
12	150	3.8	3698	4	US-09-327-536-1

13	149	3.8	4612	2	US-08-447-031A-8	Sequence 8, Appli
14	149	3.8	6168	4	US-09-071-035-457	Sequence 457, App
15	149	3.8	6168	4	US-09-071-035-461	Sequence 461, App
16	149	3.8	6168	4	US-09-071-035-465	Sequence 465, App
17	148	3.8	3827	2	US-08-447-031A-1	Sequence 1, Appli
18	147	3.7	15016	4	US-09-601-198-60	Sequence 60, Appl
19	145.5	3.7	2793	1	US-08-703-9647-1	Sequence 1, Appli
20	142	3.6	2793	4	US-09-134-001C-2477	Sequence 2477, Ap
21	139	3.5	3695	4	US-09-071-035-419	Sequence 419, App
22	139	3.5	3840	4	US-09-071-035-417	Sequence 417, App
23	139	3.5	7101	1	US-08-480-604A-9	Sequence 9, Appli
24	139	3.5	7101	2	US-08-405-496A-9	Sequence 9, Appli
25	139	3.5	7101	3	US-08-915-136-9	Sequence 9, Appli
26	139	3.5	7101	4	US-08-957-310-9	Sequence 9, Appli
27	139	3.5	7101	4	US-10-011-366-9	Sequence 9, Appli
28	138	3.5	2682	2	US-08-867-941-7	Sequence 7, Appli
29	138	3.5	2682	3	US-09-074-658-7	Sequence 7, Appli
30	138	3.5	7641	2	US-08-867-941-6	Sequence 6, Appli
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32	137.5	3.5	37948	3	US-09-251-645-11	Sequence 11, Appli
33	135.5	3.4	4565	3	US-08-776-265-1	Sequence 1, Appli
34	135.5	3.4	20986	4	US-08-961-527-54	Sequence 54, Appli
35	134	3.4	3057	4	US-09-601-198-55	Sequence 55, Appli
36	133.5	3.4	1878	4	US-09-697-064-1	Sequence 1, Appli
37	133	3.4	3288	4	US-09-107-532A-201	Sequence 201, App
38	132	3.3	2037	3	US-08-913-942-14	Sequence 14, Appl
39	132	3.3	2079	4	US-09-268-347-25	Sequence 25, Appli
40	132	3.3	580073	4	US-08-545-528D-1	Sequence 1, Appli
41	131.5	3.3	3894	3	US-09-107-532A-898	Sequence 898, App
42	131	3.3	1983	4	US-09-107-532A-9061	Sequence 3061, Ap
43	131	3.3	4376	1	US-08-119-125A-1	Sequence 1, Appli
44	131	3.3	6744	1	US-08-119-125A-2	Sequence 1, Appli
45	130.5	3.3	2570	2	US-09-056-075-2	Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-09-107-532A-864  
; Sequence 864, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEOTIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Atinello, Pamela Deneka  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 864:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2187 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: circular  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Enterococcus faecium  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (b) LOCATION 1...2187  
 SEQUENCE DESCRIPTION: SEQ ID NO: 864:  
 US-09-107-532A-864  
 Alignment Scores:  
 Pred. No.: 3,43e-09 Length: 2187  
 Score: 182.00 Matches: 155  
 Percent Similarity: 34.82% Conservative: 103  
 Best Local Similarity: 20.92% Mismatches: 238  
 Query Match: 4.61% Indels: 245  
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 Db 520 -----TCTATTTCATAGAGAAATACCATCAAGAG 551  
 QY 103 rtyrglnvaltyrcyspheasnleuylsalsalpheproleuglseraspserserVa 123  
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 RESULT 2  
 US-08-867-941-2  
 : Sequence 2, Application US/08867941  
 : Patent No. 5977337  
 : GENERAL INFORMATION:  
 : APPLICANT: Loosmore, Sheena M  
 : APPLICANT: Du, Kun-Pan  
 : APPLICANT: Wang, Qui-Jun  
 : APPLICANT: Yang, Yan-Ping  
 : APPLICANT: Klein, Michel H  
 : TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA  
 : NUMBER OF SEQUENCES: 67  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Sim & McBurney  
 : STREET: 6th Floor, 330 University Avenue  
 : CITY: Toronto  
 : STATE: Ontario  
 : COUNTRY: Canada  
 : ZIP: M5G 1R7  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patentin Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/867,941  
 : FILING DATE: 03-JUN-1997  
 : CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Stewart, Michael I  
 : REGISTRATION NUMBER: 24,973  
 : REFERENCE/DOCKET NUMBER: 1038-681 MIS:jb  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (416) 595-1155  
 : TELEFAX: (416) 595-1163  
 : INFORMATION FOR SEQ ID NO: 2:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 2694 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: single

: TOPOLOGY: linear  
 : US-08-867-941-2  
 Alignment Scores:  
 Pred. No.: 1.28e-08 Length: 2694  
 Score: 178.00 Matches: 171  
 Percent Similarity: 31.48% Conservative: 118  
 Best Local Similarity: 18.63% Mismatches: 305  
 Query Match: 4.51% Indels: 324  
 DB: 2 Gaps: 42  
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 QY 24 LysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43  
 Db 274 GCACAAAGACCGCGCTGCCGACAGGTTTGTGTGATG----- 312  
 QY 44 MetValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsn 63  
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 Db 466 GACATCAAAACCTGTATTTAACAAATCCCTGATGCTGTGATTTGATTTGATTTGATTTGAT 525  
 QY 99 GluLysSerArgSerTyrGlnValTyrCysPheAsnLeuLysValAlaPheProLeuGly 118  
 Db 526 GAACGCCACCGT---TTTGACCCCAAAAGCTAAACGATTAAGTGTATGTTATGCG 582  
 QY 119 SerAspSerValLysLys-----TrpTyrLysLysHisAspGlyIleSerThrLys 136  
 Db 583 AACTTAACAAACCTCTAAACAAACACTTACATCATCATCAGCAAGCTGATATATAG 642  
 QY 137 PheGluAspTyrAlaMetSerPro-----ArgIleThr 147  
 Db 643 AAAATATACAAAGCTGTGACCTTATGAAATATCCGTTTGGGTATCTGAACCTACAA 702  
 QY 148 GlyAspGluLeuAsnGlnLys----- 154  
 Db 703 GGAAGCACTGTACCAAAAAAATGCCGATCTCCAAATGCAAAAGACCGCATTTCCCAA 762  
 QY 155 ---LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly 173  
 Db 763 CCCATGCCCATTTTCTTTATCAGCA-----GAAACGCCAGAGACCGACTGCCCACT 816  
 QY 174 LeuGluProLeuAsn----- 178  
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 QY 179 AlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn 198  
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 QY 219 Leu----- 219  
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QY 453 ----- 453
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Db 1903 CAAACCCCAACACGAGTATATTTTGTGCAAGCGGTAGAGGACAGATACACACACGCTG 1962
QY 480 LysHisIleLysValIle----- 486
Db 1963 CCCAAGGACGATAATTCACCTTACACAGGCTTTGGCAGGCTATCTTATCCAAAAAAG 2022
QY 487 GluLysGlyTyrArgGlyLysGlyGlnAlaIleGluTyrSerGly----- 501
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QY 502 LeuThrGlnThrGlnLeuArgAlaIleThrGlnLeuAlaIleTyrTyrPheThr----- 519
Db 2083 TTAAACCGAAGAC-----TTTCCACCCAGAA 2106
QY 520 -----AspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe 535
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Db 2167 GATGATTTG-----ATTGATCTGATGATGATCACAAGAT 2199
QY 556 SerAsnProGlnLeuThrAspLeuAspPhePheLeuProAsnAsnLysTyrGln 575
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QY 609 -----ArgLysThrValThrGlyLeuAlaGly 617
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Db 2476 GCGCTTACCCCAAGGCGATGTGCCAAACTATCGTGAAGAAAGTGGGT----- 2523
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QY 678 ValLysGluThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluValAla 696
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Db 2614 CAGTTACATGACGACAAAGCGATGGCATCATGACACCGCCGAAAAAGCAGGG 2667

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RESULT 4  
 US-08-867-941-1  
 ; Sequence 1, Application US/08867941  
 ; Patent No. 5977337

```

GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M
APPLICANT: Du, Run-Pan
APPLICANT: Wang, Quijun
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867, 941
FILING DATE: 03-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-681 MTS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-867-941-1
Alignment Scores:
Pred. No.: 7,03e-08 Length: 7650
Score: 178.00 Matches: 171
Percent Similarity: 31.48% Conservative: 118
Best Local Similarity: 18.63% Mismatches: 305
Query Match: 4.51% Indels: 324
Gaps: 42
US-09-494-297-2 (1-757) x US-08-867-941-1 (1-7650)
QY 4 ThrArgPheProAsnLysLeuAsnThrLeuAsnThrGlnArgValLeuSerLysAsnSer 23
Db 375 ACAACGTACCCCAATATGCGATTAACCAACCACTGACACAA----- 413
QY 24 LysArgPheThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
Db 414 GCACAAAGACCGCGCTGCGCAGGCTTTTGTGATG----- 452
QY 44 MetValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsn 63
Db 453 -----GGTAAATTCGTGATACCAAGCCCAAAAAAT--GAC 485
QY 64 ProAspSerSerGlu-----TyrArgTyrGly-----TyrGluSerTyrVal 79
Db 486 CCAAGTATATGCAATATGATTAGTACACAGCATGCGCAAGCAAAATTAATATGTGATATGAT 545
QY 80 ArgGlyHisPro----- 83
Db 546 GCCCATGCCCCAGATGCGCATGCGCACAGTAAAACTTGCGTACGCCCATCAGCCCAAT 605
QY 84 -----TyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu 98
Db 606 GACATCAAAACCTTGATTTTAAACAAATTCCTGCAATGTGTGATTTGCAATTAGACAGT 665

```

OY	99	GluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysAlaPheProLeuGly	118
Db	666	GAAGCCACCGT---TTTGACCCCAAAAAGCTAAACACATTAAAGTATGGTATGGC	722
OY	119	SerAspSerSerValLysLys-----TriPyrLysLysHisAspGlyIleSerThrLys	136
Db	723	AACCTTAACACACCCCTCTAAACACACACTTACATCATCATCAGCAAGCTGATATATAG	782
OY	137	PheGluAspTyrAlaMetSerPro-----ArgIleThr	147
Db	783	AAAATATACAAACCGCTGTGGACCTTTATGAAATATCCGTTTGGTATCTTGAACTACAA	842
OY	148	GlyAspGluLeuAsnGlnLys-----	154
Db	843	GGAAGCAGCTGACCCCAAAAAATGCGGATACCTCCAAATGACAAAGACCGATTCCCAA	902
OY	155	---LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly	173
Db	903	CCCATGGCCATTGTGTTTATCAGCA-----GAAACGGCAGCAGCCAGCTGCCAGT	956
OY	174	LeuGluProLeuAsn-----	178
Db	957	GCTGTAAATTTAACTACACAGGCAACGCGCTGATCCCTTAAGTATGATCAAAAAACGCCCT	1018
OY	179	AlaIleArgValThrGlnGluAlaValTyrPyrTyrSerAspAsnAlaProIleSerAsn	198
Db	1017	GCACCTTCAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1076
OY	199	ProAspGluSerPheLysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSer	218
Db	1077	-----GAGGCGCATGCTGCAGTGCAGCCGCCACCATTTAT	1109
OY	219	Leu-----	219
Db	1110	CTAAACGGCTTCAATATAGCACACAGCCCTGCCACTATACGGTGAGATTGGACACAAC	1165
OY	220	---MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys	238
Db	1170	TCATTAAACGGCAAGCTGTCTTATTATGACAAATCCCAACGCAACACTGCCCAAGCCAA	1222
OY	239	GlnValProAspAspPhe-----GlnLeuSerIlePheGluSer	251
Db	1230	TACATCAAAAAGCCATTGTGACATCACCAAAAAGTCAATGAAACGATGATATCAAAATT	1288
OY	252	GluAspLys-----GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyLys	269
Db	1290	GATGCCAATAATCAACGGCAACCGCTGCTGCGTACGGCCCAATCTTGTGTTATATAGAAC	1349
OY	270	Leu-----ValProThrLysProProThrProGlyAspPro	281
Db	1350	ACAAACAAACCGACCTTTATCAAGAGAGCTGTTCACAAAAGCAACCAATCCCAATACCA	1408
OY	282	ProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGly	301
Db	1410	-----AACCTTAT-----	1418
OY	302	AspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSer	321
Db	1419	-----TCAGACACGCTAGAGGCGGCTTTATGCTGAGTGGGCGAGTACGACTG-----	1466
OY	322	PheGlnAlaArgValPheSerSerAsnAsp-----IleGlyGluArg	335
Db	1467	-----GCGGGTAAATTTTATTCATATGACAAACGATCTTATGTGCGCTTTGGTGGTAAA	1520
OY	336	IleGluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer	355
Db	1521	CGAACAACAAACGACAAACCTGTGCGCACAAAAAACGCGTATTTTATAGCGAGGCTTTGAA	1580
OY	356	IleIleArgLysPheThrPheLysValGlnIleArgLysValTyrThrIleIleAspGly	375
Db	1581	-----AAACCTACCCACAGTTTGTGGATATATGAACAGATTGGCAGATTTATTAACAGC	1634
OY	376	LysGlnIleIleGluAsnProAsnLysGlnIleValGlu-----ProTyrSerVal	391

Db	1635	AAAAAGTTAAATGATGCGCGTGAATCAGAAATTTGATTAATGCTGATATTCTTACCAAGTCAT	1694
QY	392	GIuIaIaTYrAsnAspHe-----GluGluPheSerValLeuThrThr	405
Db	1655	GACCGCTATGATGAAATTTCTTTGGGGCGCAAAAAAACCAGAAATTCACCAAAAAAGCTCAGC	1754
QY	406	GlnAsn-----TyrAlaIysPheTyrTyrAlaIys	415
Db	1755	AGCAGCACCCCAAGCGCGTCAGCTTATTTTGGCAACAGATGATTAATTTTATTTT-----	1808
QY	416	AsnIysAsnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro	435
Db	1809	-----AATGCGCACTATTATGACCTTATGACCCAGACAGCTGTGTGATAAATTTGGCCCTGCC	1862
QY	436	AspSerGlnAspGlyGlyLysThrMetThrProAspPheThrThrGlyGluVal-----	453
Db	1863	GATGCTGTCAAAAGCCCAACCAATCCATTAAGAAAAATACCTTAATGCCACACTAAATAG	1922
QY	453	-----	453
Db	1923	GACAAACCAAGTTACCGGCATCGTGTACAAAGCCAAAGATTAATACCTTTATACGCC	1982
QY	454	-----LysTyrThrHisIleAla---GlyArgAspLeuPhe-----	464
Db	1983	ATTGCGCCAAAGACTATACAGCACATCAGTTTGGCGAGAGCGCTATTAACGATGCCAAC	2042
QY	465	-----LysTyrThrValLysProArgAspThrAspProAspThrPheLeu	479
Db	2043	CAAAACCCCAACCGCAGTTATTTGTGCAAGCGCGGTAGGCGAGATACAGCACCGCCTG	2102
QY	480	LysHisIleLysLysValIle-----	486
Db	2103	CCCAAGCGAGTAATTCACCTTACACCGCTCTTTGGCAGCGCTATTCACAAAAAAG	2162
QY	487	GluLysGlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGly-----	501
Db	2163	GACAAAGGTTATAGCAATATGAGAAGAAACCATCAAGAAAAAGCCATCAAGATTATCTG	2222
QY	502	LeuThrGluThrGlnLeuAlaAlaThrGlnLeuAlaIleTyrTyrPheThr-----	519
Db	2223	TTAAACCGAAGAC-----TTCACCCCGACAG	2248
QY	520	-----AspSerAlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPhe	535
Db	2247	GATGATGCAGATGATTGACCGGCATCTGATGATTCACAAAGATGATGATGCACATGGCGAT	2306
QY	536	GlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAsp	555
Db	2307	GATGATTTTG-----ATTGCATCTGATGATTCACACAGAT	2339
QY	556	SerAsnProProGlnLeuThrAspLeuAspPheHeIleProAsnAsnAsnLysTyrGln	575
Db	2340	GATGCACGACATGGCGATGACAGATTCACATATTTTG-----GGTGAATGCGACAGATGAC	2393
QY	576	SerLeuIleGlyThrGlnThrPheIleProLysPheLeuValAspIleIleArgMetGlnAsp	595
Db	2394	GCCGCGCGACGACAAAGTATGATCATGACAGTAAAT-----ATTGCGCCTGAATTT	2441
QY	596	LysLysGlnValIleProVal-----ThrHisAsnLeuThrLeu-----	608
Db	2442	CAAAACAAATATCTGGCCCATTAATAGAGCTACTGATGAAAAACCTTTGCCCTAGATGGT	2501
QY	609	-----ArgLysThrValThrGlyLeuAlaGly	617
Db	2502	AAAAATAAAGCTAAAGTTGATGTGGATTTTGACACCAACACCTTAACGTAAATTAAC	2561
QY	618	AspArgThrLysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeu	637
Db	2562	GATGAGAGAGGTGATATCGTCTTTGATATTC-----AAAAATGGCAAAATTTGATGGCACA	2615
QY	638	SerGlnThrValLysThrAspLysThrLysLeuGluPheLysAspGlyLysAlaThrIle	657

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Db      2616  GGCCTTACCAGCCCAAGCCGATGTGCCAACAATCGTGAAGAAGTGGT----- 2663
QY      658  AsnLeuLySHISgLyGluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeu 677
      |||  |||
Db      2664  AACACCAAGGTGGC-----GGTTCTCTATACAAC 2693
QY      678  ValLySGluThrAspSerGlnGlyTyrIryValLySAlaSnSerGlnGlyAla--- 696
      ::|||::|||  |||  |||
Db      2694  ATCAAAAGATTGATGTCAGAGGCGCAATTTTTGGCACAAATGGCGGAAGACTTGGCAGGG 2753
QY      697  -----AsnAlaThrValSerLySerThrGly 704
      |||  |||  |||  |||
Db      2754  CAGTTACAGTACGACAAAGCGCATGCGATCATGACACCGCCGAAAGACAGGG 2807

RESULT 5
US-09-074-658-1
: Sequence 1, Application US/09074658
: Patent No. 6184371
: GENERAL INFORMATION:
: APPLICANT: Loommore, Sheena M
: APPLICANT: Run-Pan Du
: APPLICANT: QuiJun Wang
: APPLICANT: yang, Yan-Ping
: APPLICANT: Klein, Michel H
: TITLE OF INVENTION: LACTOFERRIN RECEPTOR GENES OF MORAXELLA
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Slim & McBurney
: STREET: 6th Floor, 330 University Avenue
: CITY: Toronto
: STATE: Ontario
: COUNTRY: Canada
: ZIP: M5G 1R7
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/074,658
: FILING DATE: 08-MAY-1998
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Stewart, Michael I
: REGISTRATION NUMBER: 24,973
: REFERENCE/DOCKET NUMBER: 1038-795
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (416) 595-1155
: TELEFAX: (416) 595-1163
: INFORMATION FOR SEQ ID NO. 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7650 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-09-074-658-1

Alignment Scores:
Pred. No.: 7.03e-08 Length: 7650
Score: 178.00 Matches: 171
Percent Similarity: 31.48% Conservative: 118
Best Local Similarity: 18.63% Mismatches: 305
Query Match: 4.51% Indels: 324
DB: 3 Gaps: 42
US-09-494-297-2 (1-757) x US-09-074-658-1 (1-7650)
QY      4  ThrArgPheProAsnLyLeuAsnThrLeuAsnThrGlnArgValLeuSerLyAsnSer 23
      |||  |||  |||  |||
Db      375  ACAACTGACCAATATGGCGATACCAACCACTGACACAA----- 413
QY      24  LysArgPheMetThrValThrLeuValGlyValPheLeuMetIlePheAlaLeuValThrSer 43
      ::|  |||  |||  |||

```

Dd	414	GCACAAAGACCGCCGCGCCGACAGGTTTTTGGATG	452
Oy	44	MeValGlyAlaLysThrValPheGlyLeuValGluSerSerThrProAsnAlaIleAsn	63
Dd	453	-----GGTAAATTCGTGATACCAAGCCCAAAAAT---GAC	485
Oy	64	ProAspSerSerGlu-----TyrArgTrpTyrGly-----TyrGluSerTyrVal	79
Dd	486	CCAGATTATACCAATGATTAGTACAGCAGTGGCAAGCAATATATATGTTGTTATGAT	545
Oy	80	ArgGlyHisPro-----	83
Dd	546	GCCCATGCCCCAGATGGCATGGCAGCAGGTAAAAACTTCGCTCAGCCCATCACCOCAT	605
Oy	84	-----TyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeu	98
Dd	606	GACATCAACACCTGTATTTTAAACAAATTCCTCGCATGTGCTGATTTTCATTGACAGT	665
Oy	99	GluGlySerAlaGlySerTyrGlnValTyrCysPheAsnLeuLysValAlaPheProLeuGly	118
Dd	666	GAAGCGCCACCT----TTTGACCCCAAAAAGCTAAACACCATTAAGTGTATGTTATGGC	722
Oy	119	SerAspSerSerValLysLys-----TrpTyrLysHisAspGlyIleSerThrLys	136
Dd	723	AACTTAAACAACACCTCTTAAAAACACACTTACATCATCATCAGCAAGCTGATATATAG	782
Oy	137	PheGluAspTyrAlaMetSerPro-----ArgIleThr	147
Dd	783	AAAATAACAAGCCTGTGACCCCTTATGAATAATTCGTTGGTATCTTGAACTACAA	842
Oy	148	GlyAspGluLeuAsnGlnLys-----	154
Dd	843	GGAAGCAGCTGACCCCAAAAATGCGCATCTCCAAATGACAAAGACCGCATTCACAA	902
Oy	155	--LeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGly	173
Dd	903	CCCATGCCCATTTTGTTTTATCACGA-----GAATAAGCAGAGCGACCTGCCCGT	956
Oy	174	LeuGluProLeuAsn-----	178
Dd	957	GCTGTAATTTATCATACACAGCAAGCACTGCTGACTTAAGTATGTCAAAAACGCCCT	1018
Oy	179	AlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaProIleSerAsn	198
Dd	1017	GCACCTTCAGCATCAGATGATGAGTGGGGCTATCTCAATGCCAGGCGCAATCCAT	1076
Oy	199	ProAspGluSerPheLysArgIleUserLysLeuValSerThrSerGluLeuSer	218
Dd	1077	-----GAGGCGCATGTGTGTCAGTGGCGGCCCATCATTTAT	1109
Oy	219	Leu-----	219
Dd	1110	CTAAACGGCTTTCATATATATAGCACACAGCGCTGCCACTTATCAGTGGATTTTGACACAAAC	1168
Oy	220	--MetArgGlnAlaLeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLys	238
Dd	1170	TCATTAAACAGCAAGCTGCTTATTATGACATATCCCAACAGCAAACTGCCAAGCCAA	1229
Oy	239	GlnValProAspAspPhe-----GlnLeuSerIlePheGluSer	251
Dd	1230	TACATCAAAAGCCATTTGACACTRACAAAAAGTCATGAAGAACCGATGTATCAAAATT	1288
Oy	252	GluAspLys-----GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGly	269
Dd	1290	GATGCCAAATCAACAGCGCAACCGCTGCTGCGTACGGCAATATCTTGTTAATGAGAAC	1349
Oy	270	Leu-----ValProThrLysProProThrProGlyAspPro	281
Dd	1350	ACAGAAACCGCACCTTTTATCAAGAGAGCTGTCTCAAAAAAGCCAAATCCCAATAACCA	1409
Oy	282	ProMetProProAsnGlnProGlnThrThrSerValLeuIleArgLysTyrAlaIleGly	301
Dd	1410	-----AACCTTAAT-----	1418





US-09-074-658-69

Alignment Scores:

Pred. No.:	2,12e-08	Length:	2718
Score:	176.00	Matches:	164
Percent Similarity:	33.43%	Conservative:	102
Best Local Similarity:	20.65%	Mismatches:	264
Query Match:	4.46%	Indels:	266
			2
			2

US-09-494-297-2 (1-757) x US-09-074-658-69 (1-2718)

OY		84	TyrTyrLysGlnPheArgValAlaHisSerLeuArgValAsnLeuGlnLysArgSer	103
Dd		493	TATTTGGATAAATTCCCAAAATATTCGACTGTG-----CACCTAGAAAACGGCAG--	543
OY		104	TyrGlnValTyrCysPheAsnLeuLysLysAla-----PheProLeuGly	118
Dd		544	-----CANGTGTTTGATGCTTAATAAACCAATATAATCAACAATATNTGGTTATGCT	594
OY		119	SerAspSerSerValLysLys-----TrpTyrLysSHisAspGlyIle	133
Dd		595	GCATTTGCTCATCACTGCACAAAAACCACCACTACATGAATATATCAACAAGAACAACATC	654
OY		134	SerThrLys-----PheGluAspTyrAla-----MetSerProArg	145
Dd		655	AAAAACAAAAAACCGAGCGATGATTAATCAAAAATTCGTTTGGCTATATGAGCAATAGA	714
OY		146	IleThr-----GlyAspGluLeuAsnGlnLysLeuArgAlaValMet	159
Dd		715	GAGCTGACCTAAATATAAAAGGTGCACGCCACGAGCGACAGAAACCGTGCATCATTT	774
OY		160	TyrAsnGly-----HisProGlnAsnAlaAsnGlyIleMetGlnGlyLeu	174
Dd		775	TTCCACCACACCTACTTATTTATTCATGATGAGATGACGACACCACTCATGCA-----	828
OY		175	GluProLeuAsnAlaIleArgValThrGlnGlnAlaValTrpTyrTyrSerAspAsnAla	194
Dd		829	-----AACGGCGGTAAATTTGACATAGTAGAGGCCAATGGTTGATCTGCACCGATGC	879
OY		195	Pro-----IleSerAsnProAspGlu-----SerPhe	203
Dd		880	AAAAACGCCCATTTTTAGATATAAACACACATAGACATTAAGTACGACTTATTTAACTCAAC	939
OY		204	LysArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeu-----	219
Dd		940	AGAAATCAATGAAGAGCGGATTTGGTGAGTGCACACACATTTATCTAAACAGCTTTAA	999
OY		220	-----MetArgGlnAla	223
Dd		1000	TATTAACACACCCCGGCCACTTATAGCGTGACCTTATGCATAAATACCCATAAAGCCAAA	1055
OY		224	LeuLysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp	243
Dd		1060	TTGTCTTATTATGACAAACCCAAACAGAAACACGCCGATGGCGCTTATATCAAGACTCAG	1111
OY		244	Phe-----GlnLeuSerIlePheGluSerGluAspLys-----	254
Dd		1120	TTTGATATACGCACAAAAAGGTCAATAGAAACCGCATGTATAGATGATGCGCAAGATTAAAT	1177
OY		255	GlyAspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeu-----	270
Dd		1180	GGCAACCGCTTACTGCGACACGCCACAAACCTTTGATATGATATAACACCAATACCGCAGCT	1233
OY		271	-----ValProThrLysProProThrProGlyAspProprometProProAsn	286
Dd		1240	TTTGTTTAAAGACCTGTTCTCCAAAAAACCAATCCCAACCAACCA-----GACCCCACAC	1299
OY		287	GlnProGlnInThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu	306
Dd		1294	-----TCAGATACG	1307
OY		307	LeuGlnGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheGlnAlaArgVal	326

Db	1303	CTAGAGAGCGGGTTTATNGTGAGTGGCGCATGAGCTG-----	CGGGGTAA	1350
OY	327	PheserSerAsnApIle-----	-GlyGluArgIleGluLeuSer	339
Db	1351	TTTTTATTCACATGACCAACGCACTTTGTGGCTTTGGTGCCAAACGCAACCAACGACC	1410	
OY	340	AspGlyThrTrpThrLeuThrGluLeuAsnSerProAlaGlyTyrSerIleAlaGluPro	359	
Db	1411	GAACCTGCGCCACAAAACGGGTATTTTGTG---ACAGATTTGAA-----AAACC	1461	
OY	360	IleThrPheLysValGluAlaGlyLysValTyrThrIleIleAspGlyLys-----	376	
Db	1462	AGCACCGACTTTGGTGGCAATGAAGACTTGGTACTTATTTGACGGTAAACAAAGTTAAAT	1521	
OY	377	---GlnIleGluAsnProAsnLysGluLeValGluProTyrSerValGluAlaTyrAsn	395	
Db	1522	GATCAAGTCATATATCAATTAATGAAGATGAACCTGCTCCTGCTACTAATAAAGAAATATAT	1581	
OY	396	AspPhe-----	-GluGluPheSerValLeuThrThr	405
Db	1582	GAATATATATTTGTGACGACGCCAACAAACATTCACCAAAAATAAATAACGCCAGGCTCAA	1641	
OY	406	GlnAsnTyrAla-----	-LysPheTyrTyr-----	413
Db	1642	AAAAACCCGCTTTATTTTGGTCACCATGATTAAGTTTTATTTTAAATGTAACATTATTATGAC	1701	
OY	414	-----AlaLys-----AsnLysAsnGlySerSerGlnValValTyrCysPheAsnAla	429	
Db	1702	TTATCAGCGCAAGAAGCAAAACACCTTGGTGTCTCCCAAGATACCAGCACCATAAAGAGT	1761	
OY	430	AspLeuLysSerProProAspSerGluAspGlyLysIleThrMetThrProAspPheThr	449	
Db	1762	ATTTTGGCTAATATCCACGATGCC-----AAAGTAACACAGACAAATAAAGTT	1809	
OY	450	Thr-----	-----	450
Db	1810	ACCAAAATCGTTTACACACCAAGCAAGATTAAGCCGTATACGCCCATTCATGCCAAAACG	1869	
OY	451	-----	-GlyGluValLysTyrThrHisIleAlaGlyArgAspLeuPhe	464
Db	1870	TATGACCAACATCATGTTTGGTGAGGTATTGTATATGATTAACAAAGCAACCCAAACGCG	1929	
OY	465	LysTyrThrValLysProArgAspThrAspProAspThrPheLeuLys-----	480	
Db	1930	AGTATATTTTGTGCAAGCGGTCAAGCGGATGCTACGTACGTCGCCAGTCGACGTAA	1989	
OY	481	-----	-HisIleLysLysValIleGluLysGlyTyrArg	491
Db	1990	TTTACCTATATATGTCCTTTTGGCAGCGCTACTGACCCAGCAAAAAGCAAAAGGTTTATAGC	2049	
OY	492	GluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaIaThr	511	
Db	2050	AAAAGATGAGATACCATCAAGCAAAAAGGCTTAAAGAT-----	2088	
OY	512	GlnLeuAlaIleTyrTyrPheThr-----	519	
Db	2089	-----TATATATTGACCAAAAGACTTTATCCCAAGATGACGATGACGATGAC	2136	
OY	520	AspSerAlaGluLeuAspLysAspLysLeuLysAsp--TyrHisGlyPheGlyAspMet	538	
Db	2137	GATAGTTTGAACCGCATGTGATGATTTCCACAGATGATATATACACATGCGCATGATGATTGG	2196	
OY	539	AsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnPro	558	
Db	2197	-----ATTGCATCTATATATTCACAAAGATGATGACACA	2229	
OY	559	ProGlnLeuThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeuIle	578	
Db	2230	GATGCGCATGACGATTTCAAGTATTG-----GGTATGGTGCAGATGATGACGCCGCA	2283	
OY	579	GlyThrGlnTrpHisProGluAspLeuValAspIleIleArgMetGluAspLysLysGlu	598	

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Db      2284 GCGAAGTGTATCATGCAGTAAT-----ATTGCCCTGAAATTGAAAAACAA 2331
QY      599 ValIeProVal-----ThrHisAsnLeuThrLeu----- 608
Db      2332 TACTTGCCCATTAATGACCTACTCATGATAAAAAAAGCTTGGCCCTAGATGTAAATAATAG 2391
QY      609 -----ArgLysThrValThrGlyLeuValaGlyAspArgThr 620
Db      2392 GCTAAGTTTGATGTAACCTTTGACACCAACAGCCCTACTGGTAATTAACGATGACAGGA 2451
QY      621 LysAspPheHisPheGluIleGluLeuLysAsnAsnLysGlnGluLeuLeuSerGlnThr 640
Db      2452 GGTATATACGTCTTGATATATC-----AAAAATGCAAAATTTGATGGCAGACAGATTTTACC 2505
QY      641 ValLysThrAspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLys 660
Db      2506 GCCAAGACCCGATGTGCCAACTATCTGTGAAGAGAGTGGT-----AACCAACCA 2553
QY      661 HisGlyGluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGlu 680
Db      2554 GGTGGC-----GGTTCTTATACACATCAAGAT 2583
QY      681 ThrAspSerGluGlyTyrLysValLysValAsnSerGlnGluVala 696
Db      2584 ATTGATGTTAAGGGCAATTTTGGCACAAATGGCGAAGAGTTGGCA 2631

RESULT 7
US-09-071-035-403
: Sequence 403, Application US/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071.035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brooks
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 403:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4249 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-09-071-035-403

Alignment Scores:
Score: 1.72e-06 Length: 4249
Percent Similarity: 34.83% Matches: 159
Best Local Similarity: 21.06% Mismatches: 326

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Query Match: 4.08% Indels: 166
DB: 4 Gaps: 40
US-09-494-297-2 (1-757) x US-09-071-035-403 (1-4249)
QY      39 AlaLeuValThrSerMetValGlyAlaLysThrValPheGlyLeuValGluSer----- 56
Db      1451 TCATTAACTACACCGTAAATGGTCCCTAATAAGCCATTCATTAATGATCCGATCAATAT 1510
QY      57 ---SerThrProAsnAlaIleAsnProAspSerSerGlyTyrArgTyrGlyTyr 75
Db      1511 ATTGACCAATTAAGTGTGTAATCC---TTGAATGCTGAAACGCTGGGATTAATAT 1567
QY      76 GluSerTyrValArgGlyHisProTyrTyrLysGlnPheAlaValAlaHisAspLeuArg 95
Db      1568 GATCAA-----AATGGTCCATTCATCAAGA 1594
QY      96 -----ValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLysLys 113
Db      1595 ACAACTGCTCAGTTATGGGAAGCAAGAACGCGATTCAAAATTTGAATTAAGTA 1654
QY      114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrLysLys 129
Db      1655 AAGCATCCTAATTATCTTCAATTACGACCTCAAAAGAAATTTATTTATTACAG--- 1711
QY      130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149
Db      1712 -----TTAGCAGC-----GATTATACAGTACGCCAACGTCAGATGGTTCA 1753
QY      150 GluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlnHisProGlnAsnAlaAsnGly 169
Db      1754 GTTATTAGTTCACACACCCCAATTAACCAAGCAATTCCAATTGCTGTTAATTAT 1813
QY      170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184
Db      1814 GTGCCAGTACTTGGCCAAAGATAAAGTATCCAGCTACGATACGATCCGATTAACAATG 1873
QY      185 GluAlaValIleTyrTyrSerAspAsnAlaProIleSerAsnProAspGluSerPheLys 204
Db      1874 AGTCGTGAAGGTTTAACCTCCAGTTGATACGACAGTAACCTACT-----AATGATGTA 1924
QY      205 ArgLysSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224
Db      1925 CGTGTTCTGAAACGACACTTCAAAAGTAAATCAATTCCTTGCAATGACAGCAAT 1984
QY      225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPhe 244
Db      1985 GATTCTTTGACTCACTAAGCGCTCGTCAAAAATTCACAGCTGGCGCC-----GATGTT 2038
QY      245 GlnLeuSerIlePheGluSerGluAspLysGlyLysPheLysGlyTyrGlnAsn 264
Db      2039 CTTTGTGACATTTATGATGATTTCAAC-----GATCGAGTATGATCAATTTATCCACAA 2092
QY      265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheMetPro 284
Db      2093 TACGGGACCGCGGCATACTTGTATTAACCAATGACGCCAACGCCGCGATATGCCA 2152
QY      285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296
Db      2153 ACGATTACTTTTGACGAAATATCAAAATGATGATACAGTTGATTTGGAAAAACCAACAA 2212
QY      297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGlnGlyAlaThrLeuGln 313
Db      2213 GGTATACATTAAT---GAGTATTAATAAACGCCCAATGCGTGGATGATCCCACTTTAT 2269
QY      314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327
Db      2270 ATAACAGGACAGCAAGAACCAACATCAATATATAGAGGCTGCTGCTGCTTCT 2329
QY      328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347
Db      2330 GTTCAAAAT-----GAAGCGTTAGACATTTTGAATGACGACAA----- 2365

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QY 348 LeuanserProalaglytyrSerllealagluProlethrPhelyValgluAlagly 367
Db 2366 -----CAAGCGCGAATCCAACTTAAATAATGTAACAAACG 2404
QY 368 LysVallythr---lleleaspglylys-----glntlegluasnProasnlyglu 384
Db 2405 ACAGTAACAACAAAATAATGTAATAAACAACATCGTGTGAAAAATCCAAACGATGAA 2464
QY 385 lleValgluProtyrSerValgluAlaTyraasnphheglugluPheserValleythr 404
Db 2465 TTAAACCAAAAGGACACCAACCAATGCTCAATGATTCATTCATTCACCGTG----- 2518
QY 405 ThrGlaasnTyralaLysphetyrTyralaLysasnlysaasnlyserSerGlnVala 424
Db 2519 -----AAGCGCGCGCAAGAAATGCT 2539
QY 425 TyrcysPheasnalaaspleuLysSerProProaspSerGlnaspglylyLysThmet 444
Db 2540 TAT-----TCATTAGAGAGAGAGCTCAAAACGCGCGAAAGTCAT 2578
QY 445 ThrProspheThrThrlyglu-----VallytyrThrHisllealaglyArg 461
Db 2579 TTAAAGACTATACATTGACAGAAACATTACGATTAATACATACCGTCTCGCAAC 2638
QY 462 AspleuPhelytyrThrVallysaProaLysPheaspThrAspProaspThrPhelysHis 481
Db 2639 GCTGGCCAAATCTATACAGAAACAAACAGCTGTAACATTTGAACCAAGATGTGCT 2698
QY 482 lleLyslysaValle-----GluLys 488
Db 2699 AGCAAGAAAAAGTCACACCTGCGCCAAATCACAATTGCAAGAGGTGATGCGGAA 2758
QY 489 GltTyraArggluLysgluAlailegluTyrserylLeuthrGluThrGlnLeuArg 508
Db 2759 GGTATGTTTATTAGCAACTGCCACATTTACACGATACATACAGTAGAGTAGAAACCA 2818
QY 509 AlaAlaThrGlnLeuAlailetyrTyrrPheThrAsp-----SerAlaGluLeu 524
Db 2819 GCAATGCGAAGGTTCTTTGAACTAATGATTAATGATCAACGATACAGCAACCGAAT 2878
QY 525 AspleuAspleuLysaspyrHisglyPhegluAspmet---AsnAspSerThrLeu 543
Db 2879 ACAACAGATGAAAAAGTCATACCTCTTGATGCCATTCAGACAGGTGATTTACTTGG 2938
QY 544 AlaValaLyslleLeuValgluTyraLaglnasPheasnProProGlnLeuThr--- 562
Db 2939 CGAGTAACGAATGTACCGCAGCAATATCCGTGATGACAAG-----TATTGACAGCA 2992
QY 563 -----AspleuAspPhePhelePro----- 569
Db 2993 AAAGCATTAAGCTGTCAGAAAGAGACAAACCAATAAATTCATTAACGAACAAAT 3052
QY 570 AsnAsnAsnlystyrGln-----SerleuilegluThrGlnThrPhePro 584
Db 3053 GATCCACAGCTGTTTACAAAGTCAAAAGTTCACAGATTTATGTGCGGATTCATGAAACCA 3112
QY 585 GluAspleuValasplelleleargmetGluAspLyslys---GluValilleProValThr 603
Db 3113 GAAGAG-----AACTTTGTTTCAACACAGATTAACAAACAGGTCAACAGCTCCCTCGAA 3166
QY 604 HisAsnleuThrleuArglysthrValThrGlyLeuAlaLysaPargThrlysaPhe 623
Db 3167 -----AAATCACTGTTTCAAGTTCAGTTGATTAACANCAAGAGGCGT 3211
QY 624 HisPhegluilegluLeuLysasnAsnlysglnGluLeuLeuSerGlnThrVallyThr 643
Db 3212 TATCCATTAAGTAAAGTGAAGAGGTAAAGAAACACACCTATGTGACCGTCAAAACC 3271
QY 644 AspleuThrAsnleuGluPhelysaPsglyLysAlaThrleasnleuLysHisglu 663
Db 3272 GACCAATCTAAGTTAAGGTCAAGAT-----ACAACGATTTATGTT-----GGTAT 3319
QY 664 SerleuThrleuGlnGlyleuProGlnGlytyrSerTyrlleuValLysgluThrAspSer 683

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Db 3320 TCGTGCAA-----CCAGAA-----GATTAATTCGTTCCAGCAGACACAA 3361
QY 684 GluGlytyrLysVal-----LysValasnSerGlnleuValAlaAsnAlaThrVal 700
Db 3362 ACAGGTCACAGACGTCCTGTTGAAAAATGATGTTCAAGGAAACAGTGAAT-----GTT 3415
QY 701 SerlysthrGlyleThrSerAspGluThrLeuAlaPhegluasn 715
Db 3416 GATTAATTAAGC-----GATTATGAATTTGTCTATAAAT 3451

RESULT 8
US-09-071-035-401
: Sequence 401, Application us/09071035
: Patent No. 6448043
: GENERAL INFORMATION:
: APPLICANT: Gil H. Choi
: TITLE OF INVENTION: Enterococcus faecalis Polynucleotides and Polypeptides
: NUMBER OF SEQUENCES: 496
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/071,035
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: A. Anders Brookes
: REGISTRATION NUMBER: 36,373
: REFERENCE/DOCKET NUMBER: PB369P2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 401:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4359 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: US-09-071-035-401

Alignment Scores:
Pred. No.: 1.79e-06 Length: 4359
Score: 161.00 Matches: 159
Percent Similarity: 34.83% Conservative: 104
Best Local Similarity: 21.06% Mismatches: 326
Query Match: 4.08% Indels: 166
DB: 4 Gaps: 40

US-09-494-297-2 (1-757) x US-09-071-035-401 (1-4359)
QY 39 AlaLeuValThrSerMetValgluAlaLysThrValPhegluLysValgluSer----- 56
Db 1546 TCATTAAGTACACCTGTAATGTGCTCTAATAAAGCATTCATTAATAGTATCCGATCAATAT 1605
QY 57 ---SerThrProAsnAlaileasnProAspSerSerSerGluTyraArgThrlytyrGlytyr 75
Db 1606 ATTAGCAACCAATTAAGTGTGTTATCTCT---TTGAATGCGGAAACGCTTGCGGTATATAT 1662
QY 76 GluSerTyrrValaArglyHisProtyrTyrrLysGlnPheArgValaAlaHisaspleuArg 95

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Db 1663 GATCAA-----AATGTCCTATTTCATCAAGA 1689  
 QY 96 -----ValAsnLeuGluGlySerArgSerTyrGlnValTyrCysPheAsnLeuLys 113  
 Db 1690 ACACTGCTCTCAGTATGGAAGCAAGAAACCGATTCAAAATTTAGAAATTTAAAGTA 1749  
 QY 114 AlaPhePro-----LeuGlySerAspSerSerValLysLysTyrTyrLys 129  
 Db 1750 AAGCATCTCAATTATCTTTCATTACGAGCTACAAAAGAAATTTATTTTATTACAAAG---- 1806  
 QY 130 HisAspGlyIleSerThrLysPheGluAspTyrAlaMetSerProArgIleThrGlyAsp 149  
 Db 1807 -----TTAGAACG-----GATTATACGTAAGCCCAACGTCAGATGGTTCA 1848  
 QY 150 GluLeuAsnGlnLysLeuArgAlaValMetTyrAsnGlyHisProGlnAsnAlaAsnGly 169  
 Db 1849 GTTATTAAAGTTCATACGCCAATTAACCAAGAAATTCAAATTCCAATGGTTTAAATTTAT 1908  
 QY 170 IleMetGluGlyLeuGlu-----ProLeuAsnAlaIleArgValThrGln 184  
 Db 1909 GTGCCAGATAGTTTGCACAAAAGATAAAAGTATCCAGTCGATACGATACCGATACCAATG 1968  
 QY 185 GluAlaValTyrPyrTyrSerAspAsnAlaProIleSerAsnProAspLysSerPheLys 204  
 Db 1969 ACTGCTGAAGGTTTAACCTCAGTTCAGTACGACAGTAACACT-----AATAGTAAG 2019  
 QY 205 ArgGluSerGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeu 224  
 Db 2020 CGTGCTGTCGAAGCAACTTCAAGTACTAAATCAATTCCTTGTCAATGCACGCAAAAT 2079  
 QY 225 LysGlnLeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspHe 244  
 Db 2080 GATTCTTTGACTACTAGCGTCCGTCACAAAATTCACAGTCGGCC-----GATGTT 2133  
 QY 245 GlnLeuSerIlePheGluSerGluAspLysGlyAspLysTyrAsnLysGlyTyrGlnAsn 264  
 Db 2134 CTTTTCACATTATGATGTTTCAAA-----GATCAGTAGATTCATTATTCACAA 2187  
 QY 265 LeuLeuSerGlyGlyLeuValProThrLysProProThrProGlyAspProPheMetPro 284  
 Db 2188 TACTGGGACCGCGCAATCTTGTGATTAACCAATGACGCCCAACGCCCTGGATATCA 2247  
 QY 285 -----ProAsnGlnProGlnThrThrSerValLeuIle-----Arg 296  
 Db 2248 ACGATTACTTTGACGAAATAATCCCACTACTTACAGCTTGATTGGAAAAACCAACAA 2307  
 QY 297 LysTyrAlaIleGlyAspTyrSerLysLeu-----LeuGluGlyAlaThrLeuGln 313  
 Db 2308 CGTTACATTAT-----GAGTATATAAAACCGCAATGCGTGGTGCAGCTGCCAATCTTTAT 2364  
 QY 314 LeuThrGly-----AspAsnValAsnSerPheGlnAlaArgValPhe 327  
 Db 2365 ATTAACAGGACAGCAAGCAACCAACATCGAATTAATGAAGCGCTCTCTCGTTCT 2424  
 QY 328 SerSerAsnAspIleGlyGluArgIleGluLeuSerAspGlyThrTyrThrLeuThrGlu 347  
 Db 2425 GTTCAAAAT-----CAACGTTAGCATTTTGCAGCAACA----- 2460  
 QY 348 LeuAsnSerProAlaGlyTyrSerIleAlaGluProIleThrPheLysValGluAlaGly 367  
 Db 2461 -----CAAGCGCGCAATTCACATTTAAATAATTCACAAAAG 2499  
 QY 368 LysValTyrThr-----IleIleAspGlyLys-----GlnIleGluAsnProAsnLysGlu 384  
 Db 2500 ACAGTACACAAAATAATTTGATATATAAAACACATCGGTGAAAAATTCACACGATTGTA 2559  
 QY 385 IleValGluProTyrSerValGluAlaTyrAsnAspPheGluGluPheSerLeuThr 404  
 Db 2560 TTAAACACCAAAAGCAACCAATGCTCAATGATTGAATTCTATTACCGG----- 2613  
 QY 405 ThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLysAsnGlySerSerGlnValVal 424  
 Db 2614 -----AAGGCGCTGCCAACAAGATGCT 2634

QY 425 TyrCysPheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444  
 Db 2635 TAT-----TCATTAGAAAGACTACAAACGGTGGCAAGTCAAT 2673  
 QY 445 ThrProAspPheThrThrGlyGlu-----ValLysTyrThrHisIleAlaGlyArg 461  
 Db 2674 TTAAAGACTATATTCATGACAGAAAACATTAGCATTTGATATACATACAGTCTCTGCAAC 2733  
 QY 462 AspLeuPheLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHis 481  
 Db 2734 CGTGCCAAATCTATACAGAAACAAACAAATCGACTCTGAAACATTGACACAGATGCTGCT 2793  
 QY 482 IleLysLysValIle-----GluLys 488  
 Db 2794 AGCAAGAAAAAGTGCACACATCGCCCAATACATTAATTCAGAAAGTATGCGCA 2853  
 QY 489 GlyTyrArgGluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArg 508  
 Db 2854 GGTATTTGTTATTTAGCAACCTGCCAATTCACAGCATACAGGTAGAGATGAAACCA 2913  
 QY 509 AlaAlaThrGlnLeuAlaIleTyrTyrPheThrAsp-----SerAlaGluLeu 524  
 Db 2914 GCAATTCGCAAGGTTTCTTTGAACTAATGATTAATGTCACCCATACAGCAACCGAATTT 2973  
 QY 525 AspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMet-----AsnAspSerThrLeu 543  
 Db 2974 ACAACAGATGAATAAGGTCAATATCTCTTGTATGCCATCATACAGATGATATATCTTG 3033  
 QY 544 AlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAspProProGlnLeuThr 562  
 Db 3034 CGAGTACCAATATGACCGCAGAAATATCCGTGATGAAGAG-----TATTGACAGGA 3087  
 QY 563 -----AspLeuAspPhePheIlePro----- 569  
 Db 3088 AAGCCATTAACTGCTGTCAAAGAGCAACCACTAAATTCATTAACGAACAAT 3147  
 QY 570 AsnAsnAsnLysTyrGlu-----SerLeuIleGlyThrGlnThrPhePro 584  
 Db 3148 GATCAACAGTCGTTTACAACTCAACATTCACAGATTTATGTCAGATTCATCAAGAAACCA 3207  
 QY 585 GluAspLeuValAspIleIleArgMetGluAspLysLys-----GluValIleProValThr 603  
 Db 3208 GAAGAG-----AAGTTTCTTCAGCAACAGATTAACAGAGTCAGAGCTTCCTTCGAA 3261  
 QY 604 HisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspHe 623  
 Db 3262 -----AAATTCACCTGTTTCAGGTCAAGTTGATTAACANCAACAGAGCGTT 3306  
 QY 624 HisPheGluIleGluLeuLysAsnLysGlnGluLeuLeuSerGlnThrValLysThr 643  
 Db 3307 TATCCAAATTATTTACAGTACGACGAGGTAAAGAAACAGCTATGTGACCGTCAAAACCC 3366  
 QY 644 AspLysThrAsnLeuGluPheLysAspGlyLysAlaThrIleAsnLeuLysHisGlyGlu 663  
 Db 3367 GACCAATCTAAGTTAGAGTCAAGAT-----ACACAGATTATGCT-----GCTGAT 3414  
 QY 664 SerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAspSer 683  
 Db 3415 TCGTGGA-----CCAGAA-----GATTAATTCGTTTCACGACAGACAGAA 3456  
 QY 684 GluGlyTyrLysVal-----LysValAsnSerGlnGluValAlaAsnAlaThrVal 700  
 Db 3457 ACAGTCAAGAGCTTCCCGTTGAAAAAATGATGTTCCAGGAGCAACAGTGAT-----GTT 3510  
 QY 701 SerLysThrGlyTyrThrSerAspGluThrLeuAlaPheGluAsn 715  
 Db 3511 GATAAATATAGC-----GATTATGAATTTCTATATAAAT 3546

RESULT 9  
 US-08-851-567B-48  
 ; Sequence 48, Application US/08851567B  
 ; Patent No. 6528484

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US-09-494-297_2 (1-757) x US-08-851-567B-48 (1-5547)
OY 157 AlAvalMeTYrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGlnPro 176
    ||| ||| ||||| ||| : : : ||||| : :
Db 2386 GCACAACAATGAATGAATGTCGCCCCACAGAGGGCTTCCCGTGGTGC--GGGCTGATAT 2442
OY 177 LeuAsnAlaIleArgValThrGlnGlu--AlaValIprpyrTyrSerAsp----- 192
    : : : : : ||| ||| ||| |||
Db 2443 ATTCATATCAATGAAGAAAGACACACCGACCTATCCCGAGTGGAAACGGCGGACGGCTATTA 2502
OY 193 -----AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208
    ||| : : : ||| : : ||| : : ||| |||
Db 2503 ACCGGCGGGGTTGAATTCACACAGCGTATATCAATACACGCTTTTTCGGAGATTCGCG 2562
OY 209 SerAsnLeuValSerThr-----SerIleuSerLeuMetArgGlnAlaLeuLys 225
    ||| : : : ||||| ||| : : : ||| : : |||
Db 2563 AGTCCCGCATTAACACACCTACTATATCCGTACCATCGGCAAGGACGGCGGCTATTA 2622
OY 226 Gln-----LeuIleAspProAsnLeuAla----- 233
Db 2623 AGCCGTGATGACTTGTATCAATFACTTACTGATGTATATATCAAGGTTTTCGGCGCAATTA 2682
OY 234 ---ThrLysMetProLysGlnValProAspSerPheGlnLeu----- 246
    ||| : : : ||| : : ||| : : |||
Db 2683 ACCACCGGGATGGCGGAAGCATTTGCC--AGTATTCACAGCTACGTCAACACGGGCGCATTG 2739
OY 247 ---SerIlePheGluSerGluAspLysGly----- 255
    : : : : : ||| : : : |||
Db 2740 GAAATATGGGAAGAAATATGCCAATTCGGGGCTTATACGCCGCCAATCTTATTCAGCTGG 2799
OY 256 AspLysTyrAsnLysGlyTyrGlnAsnLeuLeuSerGlyGlyLeuValProThrLysPro 275
    ||||| ||||| ||| : : : |||
Db 2800 GACCAATATTCATTAACCGTACAGACACTTGGCGGGGTGTTCTCAATTAGTTACTACCG 2859
OY 276 ProThrProGlyAspProPheMetProProAsnGlnProGlnThrThrSerValLeuIle 295
    ||||| ||| ||| : : : |||
Db 2860 GAAACATATATTTGATGTCGACCATCGTATCGACCAACCAATGATGAGACATTTCTG 2919
OY 296 ArgLysTyrAla----- 299
    : : : : :
Db 2920 CAATCCGTACCCAAAGCCAACTTAACGCCGATACCGTCGAAGATGCCCTTATGCTTAT 2979
OY 300 IleGlyAspTyrSerLysLeuGlnGlyValaThrLeuGlnLeuThrGlyAspAsnVal 319
    : : : : : ||||| : : : ||||| : : :
Db 2980 CTGACATCGTTGGAACAAGTCGCTTAATCTTAAGTTATTAAGCGATATCAACGATATAT 3039
OY 320 AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyGlu-- 334
    ||| : : : ||| : : ||| ||| |||||
Db 3040 AATTAACGATCAAGGGCTGACCTATTTATCGACACTGAAACTGATGCGCGTGAATAT 3099
OY 335 -----ArgIleGluLeuSerAspGlyThrTyrThrLeuThr----- 346
    : : : : : ||| : : : ||||| : : :
Db 3100 TATTGGCGAGTGTGATCACAGTAATTCACACAGCGTAATTAATTCGGCGGCTATGCTGTG 3159
OY 347 -----GluLeuAsnSerProAlaGly-----TyrSerIleAlaGlnProIle 360
    : : : : : ||| : : : ||| : : : ||||| : : :
Db 3160 AGTGAATGGCATTAATATGATGTCATTCATTAACCTTATAAAGCACTATTCGCGCACTG 3219
OY 361 ThrPheLysValGluAlaGlyLysValTyrThrIle--IleAspGlyLysGlnIleGlu 379
    : : ||| : : : ||| : : : ||| : : : ||||| : : :
Db 3220 ATATATATAA-----TCCGCGCTGATCTGCTGGTGTGAACAACAAAGAGATCAACC 3270
OY 380 AsnProAsnLysGluIleValGlnProTyrSerValGluAlaTyrAsnAspPheGlu-- 398
    : : : : : ||| : : : ||| : : : |||
Db 3271 AAACAGACAGGAATAGTAAAGATGGCTATCAAACTGAACGAGTTATCGTTATGAACCTA 3330
OY 398 ----- 398
Db 3331 AAATTCGCCGATATCCGCTATGATGCGACTTGGAAATACGCCAATCACCTTGTGATGCTAAT 3390
OY 399 ---GluPheSerValLeuThrThrGlnAsn-----TyrAlaLysPhe 411
    : : : ||| ||| : : : |||

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Db      3391 AAAAAATATCCGAGCTAAAACTGGAAAAAATAGAGCCCGCGACTCTATGTGCCGGT 3450
Oy      412 TyrTyrAlaLysasn----- 416
Db      3451 TATCAAGGTGAAGATCGTCTGCTGATGTTTATTAACAACAAGACACACTAGATAGT 3510
Oy      417 ---LysasnGlySerSerGlnValValTyrCysPheAsnAlaAspLeuLysSerProPro 435
Db      3511 TATAAAACGGCTTCATGCAAGACTATATATCTTT---GCTGATATGGCATCC----- 3561
Oy      436 AspSerGluAspGlyGlyLysThrMetThrPro----- 446
Db      3562 ---AAAGATATGACCCCGACAGACAGCAATGTTTATCGGATAT 3603
Oy      446 ----- 446
Db      3604 AGCTATCAACAATTGATTAACAATATATGTCAAGAGTGAATTAACCGCTATGACAGAGAT 3663
Oy      447 -----AspPheThrThrGlyGluValLysTyr 455
Db      3664 TATGAGATTCCTTCCTCGTGAAGTAGACCGTAAAGCTATGGTGGGAGATTTATTAAGTCTC 3723
Oy      456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
Db      3724 AGCATGATATTAACGAGATATTCACACTATCAATTAACAAGCCGATCAAGTATTTA 3783
Oy      476 AspThrPheLeuLysHisIleLysValIleGluLysGlyTyr-----Arg 491
Db      3784 AAAATCTATATCTCAACCAAAATTAAGAATTTATTAATGATATGAATGAAGAGACAGAGCGC 3843
Oy      492 GluLysGlyGlnAlaIleGluTyrSerGlyLeuThrGlnGlnLeuArgAlaIaIaThr 511
Db      3844 AATCAATGATCATGATCAATTAATATGCAAACTAGTGATTAATTTATTTATTTACT 3903
Oy      512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531
Db      3904 AGCTGGGGGTCATCAATAATACGTCATTAATAGCTGATGTTTACCCGCTATACAA 3963
Oy      532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValIu 551
Db      3964 TATAGCGGA-----ACACACAGTGCATCAACGAGAGCTACTA----- 4005
Oy      552 TyrIaGlnAspSerAsnProGlnLeuThrAspLeuAspPhePheIleProAsnAsn 571
Db      4006 TTCACCGCTGACACACTTATCCA-----TCTAAGTAGAAGCTTGATTCGAGCA 4059
Oy      572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTyrP----- 582
Db      4060 AAAGCTTCTTAACCAACCAAAATGCGCGCATTTGGTATGATTAATGCTACAGACTCTG 4119
Oy      583 ---HisProGluAspLeuValAspIleIleArgMetGluAspLysGluValIle--- 600
Db      4120 AATAAAACGAGATGCTTAACCAATATATCTTTATGACTGACAGTAAGGAGACTGCTACT 4179
Oy      601 -----ProValThrHisAsnLeuThrLeu-----ArgLysThrValIaThr 613
Db      4180 GATGCTCAAGCCCAAGTAGATTAATACGTCAATTTTCCAGCAAAAGTTCAAGTATA 4239
Oy      614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626
Db      4240 CTCAAAGCGGCTGCAAGAGCAAACTTTTACCGAGATAAAGATGCTCCATTCAGCCA 4299
Oy      627 -----IleGluLeuLysAsnAsnLys 633
Db      4300 TCACCTAGCTTTGATGAATGAATTAATTAATTAATGCTTAATGAGAGCTCTGCTGT 4359
Oy      634 GlnGluLeuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652
Db      4360 CTGAATTTTATTAACACTCAAGCAGATGATGATGTTTACCGCATTTGGCGAGAGAT 4419
Oy      653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662
Db      4420 GCGCGCAAACTGGGTTATGAAGTTTCAATATTCCTGTTACCCCTCAAGTAAAGTACCAT 4479

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Oy      663 GluSerLeuThrLeuGlnGlyLeuProGlnGlyTyrSerTyrLeuValLysGluThrAsp 682
Db      4480 AATGCCCTGACCGCTCCACCAATAATGAATGTGCGCAATATATG-----CAA 4527
Oy      683 SerGlnGlyTyrLysValLysValAsnSer-----GlnGluValAlaAsnAla 698
Db      4528 TGGCAATCTTAATCGACCGGCTGAAATCTGATTTGCCCGCAGTTGTTGCCACCGCC 4587
Oy      699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718
Db      4588 ACC-----ACCGAATGATGATCAATTCGATATGAAACTCAAGAAATTCAGAGAA 4638
Oy      719 ProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIle 738
Db      4639 CCG-----CAGTTAGCAAAAGGTTTCTATGCTACGTTGCTGATTA 4677
Oy      739 AlaGlyIleSerLeuGlyIleTyrPoli 747
Db      4678 CCTCCCTAATCACTATCAACTCATGCT 4704

RESULT 10
US-08-851-567B-46
; Sequence 46, Application US/08851567B
; Patent No. 6528484
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Faltg, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: fFrench-Constant, Richard
APPLICANT: Rochelleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Cliche, Todd A.
APPLICANT: Sukhapinda, Kitisri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photobhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESS: Dow AgroSciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296, 93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 7551 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-851-567B-46

Alignment Scores:
Pred. No.: 3,97e-05 Length: 7551
Score: 152.00 Matches: 148
Percent Similarity: 33.13% Conservative: 120
Best Local Similarity: 18.29% Mismatches: 287
Query Match: 3.85% Indels: 254
DB: Gaps: 37

US-09-494-297-2 (1-757) x US-08-851-567B-46 (1-7551)
QY 157 AlaValMetYrAsnGlyHisProGlnAsnAlaAsnGlyIleMetGluGlyLeuGluPro 176
DB 2650 GCACAACAATTGATGATGTCGCCCAAGGCGTTTCGGCTTGGTC--GGGCTGATATAT 2706
QY 177 LeuAsnAlaIleArgValThrGlnGlu--AlaValTrpTyrTyrSerAsp----- 192
DB 2707 ATTCATCATAGAAAGACACGACGACCTATGCCAGTGGGAAACCGGACGCGATATTA 2766
QY 193 -----AsnAlaProIleSerAsnProAspGluSerPheLysArgGluSerGlu 208
DB 2767 ACCGCGGGTGTGATACACACAGCTAATACATTAACGCTTCTGATGATCTCGC 2826
QY 209 SerAsnLeuValSerThr-----SerGlnLeuSerLeuMetArgGlnAlaLeuLys 225
DB 2827 AGTGGCCGATTAAGCACTACTATATTCCTGTCANAGTCGCACAGCGCGGCTATTAA 2886
QY 226 Gln-----LeuIleAspProAsnLeuAla----- 233
DB 2887 AGCCGATGACTTGTATCATACTACTACTGATGATTAATAGCTTTCTCGGCAATAAAA 2946
QY 234 ---ThLysMetProLysGlnValProAspAspPheGlnLeu----- 246
DB 2947 ACCACCCGGATCGCCGACGACCATTTGCC--AGTATTCACTGTACGTCAACCGGCAATTG 3003
QY 247 ---SerIlePheGluSerGluAspLysGly----- 255
DB 3004 GAAATAGTGGAAGAAATATGCCAATTCGGGGGTTATACGCCGCCAATTTCTTATGACTGG 3063
QY 256 AspLysTyrAsnLysGlyTyrGlnAsnLeuSerGlyGlyLeuValProThrLysPro 275
DB 3064 GCAATATACATTAAGGCTACACGACTTGGCGGGGTTTCTCAATTAGTTACTACCG 3123
QY 276 ProThrProGlyAspProPheMetProProAsnGlnProGlnThrThrSerValLeuIle 295
DB 3124 GAAATATATATGATCCGACCATGCTATTCGCAACAAACAAATGATGACGATATACG 3183
QY 296 ArgLysTyrAla----- 299
DB 3184 CAATCGCTGACGCCAAAGCAATTAAAGCGGATACCGTGAAGATGCTTATGCTTAT 3243
QY 300 IleGlyAspTyrSerLysLeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnVal 319
DB 3244 CTGACACTGGTTTAAACAAGGCTATCTTAAAGTTATTAAGCCATATCAAGATATAT 3303
QY 320 AsnSerPheGlnAlaArgValPhe-----SerSerAsnAspIleGlyGlu--- 334

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DB 3304 AATACAGATCAAGGGCTGACCTATTTCAGCACTCAGTGAACATGATCGGCTGAATAT 3363
QY 335 -----ArgIleGluLeuSerAspGlyThrThrThrLeuThr----- 346
DB 3364 TATTGGCGAGTGTCACTACACTAATATTCACAGCGATTAATTCGGCTAATGCTTG 3423
QY 347 -----GluLeuAsnSerProAlaGly-----TyrSerIleAlaGluProIle 360
DB 3424 AGTGAATGGCATTAATGATTTGTCCATTAATACCTTATTAAGACATTCGCTCAAGTG 3483
QY 361 ThrPheLysValGlnAlaGlyLysValTyrThrIle---IleAspLysGlnIleGlu 379
DB 3484 ATATATATAA-----TCCGCCCTGTATCTGCTCTGGTTGGACAAAAGAGATACCC 3534
QY 380 AsnProAsnLysGluIleValGluProTyrSerValGluAlaLysAsnAspPheGlu--- 398
DB 3535 AAACAGACAGAAATATGTAAGATGGCTATCAAACTGAACAGGATTAATGCTTATGAACTA 3594
QY 398 ----- 398
DB 3595 AATTTGGCGATATCCGCTATGATGGCACTGGAAATAGCGCAATCACCTTATGATGCAT 3654
QY 399 ---GluPheSerValLeuThrThrGlnAsn-----TyrAlaLysPhe 411
DB 3655 AAAAAATATCCGACTAAAACTGAAAAAATAGACGCGCGGACTCTATTGTGCGGCT 3714
QY 412 TyrTyrAlaLysAsn----- 416
DB 3715 TATCAAGGTGATACATCGTTGCTGCTGATGTTTATTAACCAACAGACACTAGTACT 3774
QY 417 ---LysAsnGlySerSerGlnValTyrCysPheAsnAlaAspLeuLysSerProPro 435
DB 3775 TATATAAAGCGTTCAATGACAGAGCATATATATCTT--GCTGATATGACATCC-- 3825
QY 436 AspSerGluAspGlyLysThrMetThrPro----- 446
DB 3826 -----AAAGATATAGCCCGACGAGACAGACAGCAATGTTATCGGATAT 3867
QY 446 ----- 446
DB 3868 AGCTATCAACAATTTATACCAATATATGTCAGAAAGTGAATACCGCTATGACAGAGAT 3927
QY 447 -----AspPheThrThrGlyGluValLysTyr 455
DB 3928 TATGAGATTCCTTCCTCGGAAGTACCGTAAGAGCATATGTTGGGAGATATATTAAC 3987
QY 456 ThrHisIleAlaGlyArgAspLeuPheLysTyrThrValLysProArgAspThrAspPro 475
DB 3988 AGCATGATATATTAACGAGATATATCCAACTATCAATTAACAAACCGCATCAAGTATTA 4047
QY 476 AspThrPheLeuLysHisIleLysValIleGluLysGlyTyr-----Arg 491
DB 4048 AATATATATATCTCACCAAAATTAAGATATTTCAATATGATATTAAGAGACAGAAAGCC 4107
QY 492 GluLysGlyGlnAlaIleGluLysSerGlyLeuThrGluThrGlnLeuAlaAlaThr 511
DB 4108 AATCAATGCAATGTGATGAATAAATATGCAAACTAGTGATTAATTTATTTGTTACT 4167
QY 512 GlnLeuAlaIleTyrTyrPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAsp 531
DB 4168 AGCTTGGGGGTCAATCAATAATACCTGCAAAATTAACATCAATGTTTATACCCCGCTACAA 4227
QY 532 TyrHisGlyPheGlyAspMetAsnAspSerThrLeuAlaValAlaLysThrLeuValGlu 551
DB 4228 TATAGCGGA-----AACACCATGAGCTCAATCAACAGGAGACTACTA----- 4269
QY 552 TyrAlaGlnAspSerAsnProProGlnLeuThrAspLeuAspPheThrLeuProAsnAsn 571
DB 4270 TTCCACCGTGACACCACTATCA-----TCTAAAGTGAACGTTGATTCCTGAGAGA 4323
QY 572 AsnLys-----TyrGlnSerLeuIleGlyThrGlnTrp----- 582

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Db 4324 AACCTGCTCTAACCAACCAAAATGCCCATTTGGTGAATGATTATGATCAAGACTCTCTG 4383
QY 583 ---HISProGluAspLeuValAspIleIleArgMetGluAspLysGluValIle--- 600
Db 4384 AATAAACCGGATGACTTAAACATATATCTTATGACTGACAGTAAGGCACTGCTACT 4443
QY 601 -----ProValThrHisAsnLeuThrIleu-----ArgLysThrValThr 613
Db 4444 GATGCTCAAGCCCGCTGAGACTTATATCTGCAATTTCTCCAGCAAAAGTTCCAGATATA 4503
QY 614 GlyLeuAlaGlyAspArgThrLysAspPheHisPheGlu----- 626
Db 4504 GTCAAGCGGGGTGGCAAGAGCAAACTTTTACCGCAGATAAAGATGCTCCATTCAGCA 4563
QY 627 -----GlyLeuLysAsnLys 633
Db 4564 TCACCTACCTTGTGATGAATGATTCATATTAAATGCTTGAATAGACGTTCTGTG 4623
QY 634 GlngIleuLeuSerGlnThrValLysThrAspLysThrAsnLeuGluPhe---LysAsp 652
Db 4624 CTGAATTTTATTAACACTCAAGCCAGTATTGATGTTACTTTTACCAGCAATTTGCGGAGAT 4683
QY 653 GlyLys-----AlaThrIleAsnLeuLysHisGly 662
Db 4684 GCGCCCAAACTGGCTTATGAAGTTTCAGTATTCCTGTTACCCCTCAAGTAGTACCGAT 4743
QY 663 GluSerLeuThrLeuGlnGlyLeuProGluGlyTyrSerTyrLeuValLysGluThrAsp 682
Db 4744 AATGCCCTGACCTCCACCATTAATGAATGATGTCGCAATATATG-----CNA 4791
QY 683 SerGluGlyTyrLysValLysValAsnSer-----GlnGluValAlaAsnLys 698
Db 4792 TGCGAATCTTATGACCCGCTGATATCTATTTGCCCGCCAGTATGTTGCGAGCGCC 4851
QY 699 ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGlu 718
Db 4852 ACC-----ACCGAATGATGATTCAGTATGAGAAACACAGAAATTTCCAGGA 4902
QY 719 ProValValProThrGlyValAspGlnLysIleAsnGlyTyrLeuAlaLeuIleValIle 738
Db 4903 CCG-----CAGTTAGGCAAAAGTTTCTATGACTACGTTCCGTGATA 4941
QY 739 AlaGlyLysLeuGlyIleTyrGly 747
Db 4942 CCTCCCTATTAACCTATCAACTCATGT 4968

RESULT 11
US-08-714-402-1
: Sequence 1, Application US/08714402
: Patent No. 5910441
:
: GENERAL INFORMATION:
: APPLICANT: ROCHA, Claudia
: APPLICANT: FISCHETTI, Vincent A.
: TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN-BINDING
: TITLE OF INVENTION: PROTEIN FROM GROUP A STREPTOCOCCI
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/714,402
: FILING DATE: 16-SEP-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:

```

```

: NAME: McGowan, Malcolm K.
: REGISTRATION NUMBER: 39,300
: REFERENCE/DOCKET NUMBER: 016921-097
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3531 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
:
: US-08-714-402-1
:
: Alignment Scores:
: Pred. No.: 1.87e-05 Length: 3531
: Score: 150.00 Matches: 192
: Percent Similarity: 33.47% Conservative: 127
: Best Local Similarity: 20.15% Mismatches: 329
: Query Match: 3.80% Indels: 306
: Gaps: 50
:
: US-09-494-297-2 (1-757) x US-08-714-402-1 (1-3531)
:
: QY 21 LysAsnSerLysArgPheThrValThrLeuVal-----GlyValPheLeuMetIle--- 37
: Db 539 AAACACCGCGGACTTGACAGTGTATGATGAGAACGGGTATACCAAGTTGGTTGAA 588
: QY 38 -----PheAlaLeuValThrSerMetValGlyValLysThrValPheGlyLeuVal 54
: Db 569 AATCCCTTATATGGGAAATCTCAGTAAGCAGGCTCAAAAGATTT----- 636
: QY 55 GluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTrp----- 72
: Db 637 ---ACTAGTCTTACAGTTGGAATAATGCCAAATGTCAGTGTCTTAATATATGGAAA 693
: QY 73 -----TyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
: Db 694 ACAGAGGTAGTAGTGGCGCACCGGATTTCTACCGCAACATGCGCGCTATTTTAAATG 753
: QY 89 Arg-ValAlaHisAspLeuArgValAsnLeuGlnGlySerArgSerTyrGlnValTyrCy 108
: Db 754 TCTTTTGAGTTGAACAAAGATTAATCTGAACAAATCCAGCCAGTGATACCTTTGTG 813
: QY 108 sPheAsn-----LeuLys-----LysAlaPhe 115
: Db 814 TTACAGCTGATAGACGTCCTCAATCTTAAGGATACAGTCAAGATATCCCTTAATATCT 873
: QY 115 eProLeuGlySerAspSer-----SerValLysLysTrpTyrLysLysHisAspGlyIle 133
: Db 874 TACGAC-AGTGCAATTAATGCTCGCTTGGATTTGGAATAATACATGCTGAGAACCATCAACT 932
: QY 133 eSerThrLysPheGluAspTyrAla----- 141
: Db 933 TATCTATACTTTACACAGATTATATTTGCGGCTTAGATATAAGTCCAGTTGCTCGCAATT 992
: QY 142 -----MetSerPr 144
: Db 993 GAGCTTATTCCTAGAGATAAGAGAGTGTGGAATACTAGTATCTCAAAATTTTAAGAG 1052
: QY 144 CArgIleThrGlyAspGluLeuAsnGlnLys-----LeuArgAlaValMetTyrAsnGlu 162
: Db 1053 TACCATTAGTGGCGAGGATCACTATTAAGGAAGGATTATGTTTATGAAAAAGA 1112
: QY 162 YHisProGlnAsnAlaAsnGlyIleMetGluGlyLeu-----Glu 175
: Db 1113 GAGCACTTAAGAAAGCAATTATATCTAGTAATGATTTGAGCAATGTGGGTGGAGATTTGA 1172
: QY 175 uProLeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAspAsnAlaPr 195
: Db 1173 AAGTACAAACACC-----GAAACGGGAGAAATTTGCTGATGATTTATGCAATCCAAA 1226

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: Sequence 1, Application US/09327536
: Patent No. 6355477
: GENERAL INFORMATION:
: APPLICANT: FISCHETTI, Vincent A.
: TITLE OF INVENTION: FIBRONECTIN AND FIBRINOGEN BINDING PROTEIN FROM GROUP A
: FILE REFERENCE: 022927-008
: CURRENT APPLICATION NUMBER: US/09/327,536
: CURRENT FILING DATE: 1999-06-08
: PRIOR APPLICATION NUMBER: US 08/714,402
: PRIOR FILING DATE: 1996-09-16
: NUMBER OF SEQ ID NOS: 2
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3698
: TYPE: DNA
: ORGANISM: SF6BP gene
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (196)..(3681)
US-09-327-536-1

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Alignment Scores:
Pred. No.: 2.02e-05 Length: 3698
Score: 150.00 Matches: 192
Percent Similarity: 33.47% Conserved: 127
Best Local Similarity: 20.15% Mismatches: 329
Query Match: 3.80% Indels: 306
DB: 4 Gaps: 50
US-09-494-297-2 (1-757) x US-09-327-536-1 (1-3698)

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OY 21 LysanserLysArgptherhValhLeuVal-----glyValPheUmetile--- 37
DB 529 AAACACACCGGAGCTTGACAGTGTATATGAGACGGCTATACCAAGTTGGTGAA 588
OY 38 -----PheAlaLeuValhSerMetValGlyAlaLysThValPheGlyLeuVal 54
DB 589 AATCCCTAATATGGGAAATCATCTAGTAAGCAGGGTCAAAAGATGTT----- 636
OY 55 GluSerSerThrProAsnAlaIleAsnProAspSerSerSerGluTyrArgTrp----- 72
DB 637 ---AGTACTTCTTACACTTGGAAATATCCCAAAATGCTGTTTCAAAATATGGAAA 693
OY 73 -----TyrGlyTyrGluSerTyrValArgGlyHisProTyrTyrLysGlnPhe 88
DB 694 ACAGAGCTTAGTAGCGCGACGCGATTCTTACCGCAACATGCGCGCTATATTAAATG 753
OY 89 Arg-ValAlaHisAspLeuArgValAsnLeuGluGlySerArgSerTyrGlnValTyrCy 108
DB 754 TCTTTTGTGTAACAAAGATTAATCTGAACAAATCAACCCAGTGATACCTTTGTG 813
OY 108 sPheAsn-----LeuLys-----LysAlaLph 115
DB 814 TTACAGCGTGAATAGCTCTCAATCTTAAGGTATCACTCAAGATATCCCTAAATCAT 873
OY 115 eProLeuGlySerAspSer-----SerValLysLysTyrTyrLysHisAspGly11 133
DB 874 TACGAC-AGTCAATATAGTCGCTGCGATTGGAATAATACATGCTGAGAACATCACT 932
OY 133 eSerThrLysPheGluAspTyrAla----- 141
DB 933 TATCTAATCTTTCACAGATTAATATTGCGGTTTAGATAAAGTCAGTTGCTCGCAAT 992
OY 142 -----MetSerPr 144
DB 993 GAGCTTATCTCTAGAGATTAAGCAAGTGTGCAAAATCTAGTATCTCAATTTTAAAG 1052
OY 144 oArgIleThrGlyAspGluLeuAsnGlnLys-----LeuArgAlaValMetTyrAsnG1 162
DB 1053 TACATAGTGTGCGACGAGATACCTATAAAGAAAGCGTTAATGTTCTTTATGAAATGA 1112

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OY 162 yHisProGlnAsnAlaAsnGlyIleMetGluGlyLeu-----G1 175
DB 1113 GAGCACTAAAGAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1172
OY 175 uProLeuAsnAlaIleArgValhThrGlnGluValAlaTyrPyrTyrSerAspAlaPr 195
DB 1173 AAGCTACCAACACC-----GAAAGCGAGAAATTTCTGATATGTTATGCAATCCAAA 1226
OY 195 oLleSerAsn---ProAspGluSerPheLys-----ArgGluSe 207
DB 1227 CCGTACCAATATTCCTTATGCGACCATGATTAATTAATTAATTAATTAATTAATTA 1286
OY 207 rGluSerAsnLeuValSerThrSerGlnLeuSerLeuMetArgGlnAlaLeuGlyGlnLe 227
DB 1287 TACAAGCGACTTAGAAACGAGCTAATACAGATGCTGCTGAGCTTGAGAGATTACAGT 1346
OY 227 uLleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAsp----- 243
DB 1347 CTATGACGTACCTGAGAGAGAAATTTACATCAAGTATGAGGCTGATGTTACAAACT 1406
OY 244 -----PheGlnLeuSerIlePheG1 250
DB 1407 TACTTTAAGAACGATATACACAGACGCTAGAAATGTTTCAAAATGACCAACGTC 1466
OY 250 uSerGluAspLysGlyAspLys---TyrAsnLysGlyLys----- 262
DB 1467 GCGAATTAATCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1526
OY 263 -----GlnAsnLeuLeuSer----- 267
DB 1527 AACACACCAATCTGTGAATCCATTTGTTTCAATTCATTTTGGCAAGTTTCCGTGTC 1586
OY 268 -----GlyGly----- 269
DB 1587 TTCTGAATATGCTGCTTTTACTCCAGTTGGAGAAATGTTACTTCAAAAGCAATTTGC 1646
OY 270 -LeuValProThrLysProProThrProGlyAspProPheMetProProAsnGlnProG1 289
DB 1647 CTGTCTCTCTTAAAGGTAGTGTGTTGGGAAAGTGAATTT-----ACTAACCCCTC 1700
OY 289 nThrThrSerValLeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeu----- 306
DB 1701 TATTACAGTACGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1760
OY 307 -----LeuGluGlyAlaThrLeuGlnLeuThrGlyAspAsnValAsnSerPheG1 323
DB 1761 CAATGTGCATGTCGAGAAAGCGCTTTTGGAGCTGCTTCATCAATTAATTAATTAAT 1817
OY 323 nAlaArgValPheSerSerAspIleGlyGlu-----ArgIleGluLeuSerAspG1 341
DB 1818 GAAATTAAGAGCCAGTTCAAACACACAGAGAGAGTTTACTTTAAGACCTGACCTCGG 1877
OY 341 yThrTyrThrLeuThrGluLeuAsnSerProAlaGlyTyrSer----- 355
DB 1878 CACATATGACCTGTATGAACAAAGACCCCAAAAGGTATATCGACGAGTACGAGAAAT 1937
OY 356 -----IleAlaGluProIleThrPhe----- 362
DB 1938 GCGCAGCCCTTACTGTTGATACCAACCTGCTGAGGAAATGCTACCTGCTGGAAGCC 1997
OY 363 -----LysValGluAlaGlyLysValTyrThrIleAspGlyLysGln-- 377
DB 1998 ACATTCGCTGTAAAGTAGAAGCTTAACAAAGAGATGCTGCAACATTAAGAAAC 2057
OY 378 -IleGluAsnProAsnLysGluIleValGluProTyrSerValGluAlaTyrAspAsp 397
DB 2058 CCTTACGTTTTCAGGGAAGAAATTTGGAG-----AATGACAG 2096
OY 397 eGluGluPheSerValLeuThrThrGlnAsnTyrAlaLysPheTyrTyrAlaLysAsnLy 417
DB 2097 ACCAGAT-----CAACGCCACCAAGAAATTCAGAGTCAACTGTTCGA 2138
OY 417 sAsnGlySerSerGlnValValTyrCyPheAsnAlaAspLeuLysSerProProAspSe 437

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Db      2139 AAATGGTCAA-----AGATGCTTAACAGAT 2165
QY      437 RGLUASGLYGLYLSThrmethThrProaspheThrThcglyluVallystYrThrHi 457
Db      2166 TCAAGAA-----GTACGAGAGAT-----AACGATTGCTTAT---CA 2201
QY      457 sileAlaGLYARgAspleuPhelystYrThrVallysProArghsPhrasProaspth 477
Db      2202 CTTC-----AAGACTTGCTAGTACGATGCCAAGATCAGAG----- 2241
QY      477 rPheLeuLysHisIleLysLysValIleGlyLysGLYTYrArgLulysGLYAlaIle 497
Db      2242 -----TATAGTACTGCTAGTGAAGAGTAAGTTCAGACGCTCAAGGT 2288
QY      497 egluTYrSerGlyLeuThrgluThrgluLeuArgAlaIleThcGlnLeuAlaIleYrTy 517
Db      2289 GTCTATTTAGGAATATATATTAAACCCAGA--GAACAGAAATTTGTGTTGAACA 2345
QY      517 rPheThrAspSerAlaGluLeuAspLysAspLysLeuLysAspTYrHisGlyPheGlyAs 537
Db      2346 GAATTAACCTTAACCTTGAATTTGGAATGCTGAATGAATAAGTCAATCTGGTCAAAAAT 2405
QY      537 pMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTYrAlaGlnAspSer-- 556
Db      2406 CATTGATGAAGACACGCTTACGCTTCAAGATGAAGAAATTTGAAAAATGATACGCGC 2465
QY      557 -----AsnProGlnLeuThrAspLeuAspPhePhe-----IleProAs 570
Db      2466 AGAAATTCGTCCCAACCCATTCAGATGCACTTTATGTCGATGCACTGGCTGTGGAAG 2555
QY      570 AsnAsnLysTYrGlnSerLeuIleGlyThrglnTYrHisProGlu----- 585
Db      2526 TCAACCAATTTATTTCTGCTCAGTAATGAGTGTCAATTGATTAAACCTTGAA 2585
QY      586 -----AspLeuVal----- 588
Db      2586 GAAGTATTAAGAACAGATGATGATCATCTACTGATTAAAGATACTGTTCCAAC 2645
QY      589 -----AspIleIleArgMetGlnAspLysLysGluVa 599
Db      2646 AGGTTATGATGCTACTTACTCAGCTAATGATATATT-----AATACCAACGTGAGGT 2699
QY      599 Iile-----ProValThrHisAsnLeuThrLeuArgLysThrVa 612
Db      2700 TATTACACAAGAACGAGAACTAGAGATTGAAGAAACGCTCCCTAGATCAGCTGC 2759
QY      612 lThrglyLeuAlaGlyAspArgThrLysAspPheHisPheGluIleGlu----- 628
Db      2760 TTCAAGC-----GGTACCACTACTGTCGAAGACTCAGCCAGTGTATCTTATCAGG 2813
QY      629 -LeuLysAsnAsnLysGlnLysLeuLeuSerGlnThrVallysthrAspLys--ThrAs 647
Db      2814 TTATATCAGTAGCAGCAAGTACGTCGGTATGACATTAATGAAGATATGTCTACCCA 2873
QY      647 nLeuGluPheLys-----AspGlyLys-----AlaThrIleAsnLe 659
Db      2874 TATTAAATTTCTAAAACGTGATATTGCGCAAGAGTGTAGCTGTCACACTATGAGTT 2933
QY      659 ulysHisGlyGluSerLeuThrLeuGlnGly----- 669
Db      2934 GCGTGATTCATCTGGTAAACTATTTAGTACATGATTCAGATGACAGTGAAGATTT 2993
QY      670 -----LeuProGlnLysTYrSerTYrLeuVallysgluThrAspSerGluGlyTYrLy 687
Db      2994 CTACCTGATGCCAGAAATATATACATT---GTGGAACCGCAGCACACGCTTATGGA 3050
QY      687 sVal-----LysValAsnSerGlnLysValAlaAsnAlaThrValse 701
Db      3051 GATAGCAACTGCTATTACTTTACAGTTAATGAGCAA-----GGTCAGGTTACTGTAAA 3104
QY      701 rlystThrglyIleThrSerAspGluThrLeuAlaPheGluAsnAsnLysGluProValVa 721

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Db      3105 TGGCAAGCACTAAAGTGACACTATTTGTCATGGTTGAGCTTACAGCCAACTAA 3164
QY      721 lProThrgly-----ValAspGlnLysIle 729
Db      3165 GCGTTCAGCTCAGCTTATGCTATATTGTAAGAAACGCTT 3201

RESULT 13
US-08-447-031A-8
: Sequence 8, Application US/08447031A
: Patent No. 5851794
:
: GENERAL INFORMATION:
: APPLICANT: GUS, Bengt
: APPLICANT: HOOK, Magnus
: APPLICANT: JONSSON, Hans
: APPLICANT: LINDBERG, Martin
: APPLICANT: PATTI, Joseph
: APPLICANT: SIGNAS, Christer
: TITLE OF INVENTION: A COLLAGEN BINDING PROTEIN AS WELL AS
: TITLE OF INVENTION: ITS PREPARATION
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Burns, Doane, Swecker & Mathis
: STREET: P.O. Box 1404
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: United States
: ZIP: 22313-1404
:
: COMPUTER READABLE FORM.
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/447, 031A
: FILING DATE: 22-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/861,804
: FILING DATE: 21-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/SE91/00707
: FILING DATE: 22-OCT-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: SE 9003374-7
: FILING DATE: 22-OCT-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: McGowan, Malcolm K.
: REGISTRATION NUMBER: 39,300
: REFERENCE/DOCKET NUMBER: 012889-006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (703) 836-6620
: TELEFAX: (703) 836-2021
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4612 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 931..4485
:
: US-08-447-031A-8
:
: Alignment Scores:
: Pred. No.: 3.7e-05 Length: 4612
: Score: 149.00 Matches: 149
: Percent Similarity: 34.11% Conservative: 115
: Best Local Similarity: 19.25% Mismatches: 268
: Query Match: 3.78% Indels: 242
: Gaps: 41

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US-09-494-297-2 (1-757) x US-08-447-031A-8 (1-4612)

QY	99	GLUGLysERaRGserTYrGlnValTYrCYcSpheasnLeuys-----	112
Db	1735	CAAGCGTATGGGCTCATTAATAGTTTTCATTAATCAATTAACAAACAAATTCAGAAATGAA	1794
QY	113	-----LYsAlaPheProLeUGLYSerAspserSerValLYsLYsTPrTYrLYsShs	130
Db	1795	CAGCAAAAAGAGTTGTTTAATTAATTCACAAAGCT-----TGGTATCAAGAGCAT	1842
QY	131	AspGLYIleSerThLYsPheGLuAspTYrAlaMetSerProaGLIleThGLYAspGLu	150
Db	1843	GGT-----AAGAAAGAGCGAAGCGGAAATCA	1869
QY	151	LeuasnGLInLYsIleuATgAlaValMetCYrAsnGLYsProGLInAsnAlaInGLYle	170
Db	1870	TTTAATATATCTGTG-----CACAAATTAATAGCTAAATGCCGGT	1908
QY	171	MetGLUGLY-----LeuGLuProLeuAsnAlaIleArgValThrGLInGLu	185
Db	1909	ATTGAAGGTACTGTAAAGCGATGATTTAAAGTTTAAACAGCATAAAGATACCAG--	1965
QY	186	AlaValTrpTYrTYrSerAspAsnAlaProIleSerAsnProAspGLuSerPheLYs---	204
Db	1966	-----GCCTCTATACTAAT-----GTAAATTTTAAACTT	1995
QY	205	ArgGLuSerGLuSerAsnLeuValSerThrSerGLuSerLeuMetArgGLuAlaLeu	224
Db	1996	TCTAATAAAGATGGATCACTGTGTAAGACAAATCA-----AAACAAATT	2040
QY	225	LYsGLInLeuIleAspProAsnLeuAlaThrLYsMetProLYsGLInValProAspAspPhe	244
Db	2041	GAGATTTATACAGATGCAAAAGCGATATGCTAATTTTAAAGCGTTCCTAGTGGAGCATAT	2100
QY	245	GLInuSerIlePheGLuSerGLu-----AspLYsGLYAspLYsTYr---	258
Db	2101	ATTTTAAAGAAATAGAGGCCGCCACGACCGTATCATTTTGATGAATGAAGATAAAGAAATATCCG	2160
QY	259	-----AsnLYsGLYTYrGLInAsnLeuLeuSerGLYGLYleu---	270
Db	2161	TTTACTATGAAGATACAGATAAATCAGGGAATTTTACGACTAATGAAATATGCAAAACCG	2220
QY	271	-----ValProThLYsProProThrProGLYAspProPromePro	284
Db	2221	ATGAAAAAACAAGATGTTTCTGCTCAAAAAGTTTGGAAAGCCACTCAAAAAGTGAAA	2280
QY	285	ProAsnGLInProGLInThrThrSerValLeuIleArgLYsTYrAlaIleGLYAspTYrSer	304
Db	2281	CCA-----ACATTTATTTCAGTTGTCAAAACAAGATGACAAATCA	2322
QY	305	-----LYsLeuLeuGLUGLYAlaThrLeuGLInLeu	314
Db	2323	AATCAACACACCAGTAGACAAAGCAGAGATTTAAAAAATTAGAAGATGCAACACAAAAGTGG	2382
QY	315	ThrGLYsPAsnValAsnSerPheGLInAlaArgValPheSerSerAsp---IleGLY	333
Db	2383	ACATGCTCTAATCTT-----CCGAAAAATGCAAAAATATGCC	2418
QY	334	GLuArgIleGLuLeuSerAspGLYThrTYrThrLeuThrGLuLeuAsn-----	349
Db	2419	AAGGCTATTAAA-----TATTATTAAAGAAAGTAATGCTCAAGGTCAA	2463
QY	350	-----SerProAlaGLYTYrSerIleAlaGLu-----	358
Db	2464	GATCAACAACACCGAGAGATATACAAAAAACAATAGTTAGTGTACTAATATCTGAA	2523
QY	359	---ProIle---ThrPheLYsValGLInAlaGLYsValTYrThrIleIleAspGLYs	376
Db	2524	AAACCAATCGAAACAACATCATTAATGCTGCAAAAAGATATGGACGACAAAGACAAATCA	2583
QY	377	GLInIleGLuAsnProAsnLYsGLUIleValGLuProTYrSerValGLuAlaTYrAsnAsp	396
Db	2584	GATGTGTAGAGACGACAGAAAA-----GTCAGTGTGAATTTATTTGGCTAAC	2628

QY	337	PhcglugluPheSerValLeuThrThrGlnsnPylalalysPheTyrTyr-----	413
Db	2629	GGGGGAAAGATGAAAAACCTTAGACGTGACATCTGAACAAACCTGAGTACGAATTGATAA	2688
QY	414	-----AlatysAsnIysAsnGlySerSerGlnValValTyrCysPheAsnAlaSerLeu	431
Db	2689	GACCTTACCGAAGTATGATGAAAGGA---AAGAAATAGATATATACGTACCGGAAGATCAC	2744
QY	432	LysSerProProAspSerGluAspGlyLysThrMetThrProAspPheThrThryL	451
Db	2746	GTAAAGAGACTACACAAACAGACATCAACGCTGACGACAAATAGAACACAGCATATACACAGGA	2805
QY	452	GluValLysTyrThrHisIleAlaGlyArgAsp-----	462
Db	2806	GAGACATCGGCACACGTAAACAAAAATTGGGATGACATTAATACCAAGACGGAAAAACGA	2865
QY	463	-----LeuPhe-----LysTyrThrValLysProArgAsp	472
Db	2866	CCAACTGAATATCAAAAGTGGATTTATATCAAGACGGAAAAAGCAAGAAACGGACACGA	2922
QY	473	ThrAspProAspThrPheLeuLysHisIleLysLysValIleGluLysGlyTyrArgGlu	492
Db	2926	TTAAATGAGATCTAATTAAGTCAACCATCGCTGACAGAGATTAGAGAA-----AAACCA	2979
QY	493	LysGlnGlnAlaIleGluTyrSerGlyLeuThrGluThrGlnLeuArgAlaAlaThrGln	512
Db	2980	AAAGGACACAAAGTAATATACACATCGACGAATTAACAAAGTCMAAGTTATTCACAA	3033
QY	513	-----IeuAlaIleTyrTyrPheThrAspSer	521
Db	3040	CATGTGGATTAACAATATGATGGTATGCTTGTATGGACAAATTAATATATACCCACAAACCA	3093
QY	522	AlaGluLeuAspLysAspLysLeuLysAspTyrHisGlyPheGlyAspMetAsnAspSer	541
Db	3100	ACATCAATTTAGTGGTGAATAAGTATGGAGAC-----GACAAAGACAT--	3141
QY	542	ThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSerAsnProGluLeu	561
Db	3142	-----CAAGATGGTAAAGACACAGAAAA	3165
QY	562	ThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSerLeu-----Ile	578
Db	3166	GTCAGTGTGAAT--TTATGTGCTGATGAGAGAAAGTAAAAACCTTAGACGTGACATCT	3222
QY	579	GluThrGlnTyrPheHisPheGluAspLeuValAspIleIleArgMetGlnAspLysGlu	598
Db	3223	GAACCAAACTGCAAGTACGAA---TTTAAACACTTACCGCAAGTATGATGAAAGAAAGAAA	3275
QY	599	ValIleProValThrHisAsnLeuThrLeuArgLysThrValThrGlyLeuAlaLysP	618
Db	3280	ATA-----GAATATACAGTGCAC-----CAAGAT	3303
QY	619	ArgThrLysAspPheHisPheGluLeu-----	627
Db	3304	CACGTAAAGACTACAAACACACATCAACCGGTACGACAATTAACGACAAAGTATACACCA	3365
QY	628	-----GluLeuLysAsnAsnLysGlnGluLeu	636
Db	3364	GGAGAGCAATGGCGCAACAGTAACAAAAATTGGATGACATTAATTAACCAAGACGGAAAA	3422
QY	637	LeuSerGlnThrValLysThrAspLysThrAsnLeuGluPheLeuAspGlyLys-----	654
Db	3424	CGACCAACTGAATATCAAGTTGAGTTA-----TATCAAGACGGAAAAACCAACA	3471
QY	655	-----AlaThrIleAsnLeuLysHisGlyLysSerLeuThrLeuGlnGlyLeu---	670
Db	3472	GGAAAAAGCGCAACCTTAATGAATCTTAATAGTGGACCCATAGCTGACACAGATTAAGAT	3533
QY	671	-----ProGluGlyTyrSerTyrLeuValLysGlu---ThrAspSerGlnGly	685
Db	3532	GAAAAAGCAAAACCCACACACTTAATATATATACAGTCCGAGAAATTTAAACAAAGCTCAAAAGGT	3591



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Db 4402 ACAGCCTATTATTAATACACAGCCAGTCCCATTTGAAATTGTCAGAAAAATGCTGCT 4461
Oy Lys-----ValThrIle 372
Db 4462 AAACACGGCGTCGCTGCTAGTACAACTTTGAGTTACAAAGGGCTTTCGAAATC 4521
Oy 373 IleAspGlyLysGlnIleGluAsnPro----- 381
Db 4522 GTGAAACAGAAATAGCGCAGACCAACCATTTAGCAGTGTCTTTTGAATATATGATCAC 4581
Oy 382 AsnLysGlnIleValGlnProTyrSerValGlnAlaTyrAsnAspPheGluGlnPheSer 401
Db 4582 AATAAACA-ATCATTAGGATATACAG-----AACGAGTGCAGAAAGTGC--- 4625
Oy 402 ValLeuThrThrGlnAsnTyr-----AlaLysPhe-TyrTyrAlaLysAs 416
Db 4626 -----CAAATATATCTTTAGAGACTTGGCGCAGGTACTTATATATACAAAGA 4673
Oy 416 n-----LysAsnGlySerSerGlnValValTyrCys----- 426
Db 4674 AATCAACAGCACCAAAATTAACAGATGGCGCAGATTAATTTATTCCTGCAATTAGTAAA 4733
Oy 427 -----PheAsnAlaAspLeuLysSerProProAspSerGlnAspGlyLysThrme 444
Db 4734 AGTAGAAATTCGTGATTCATCAAGGTGATCCGAGATT----- 4773
Oy 444 tThrProAspPheThrThrGlyGlnValLysTyrThrHisIleAlaGlyArgAspLeuPh 464
Db 4774 -----TTCCAAATAGGG-----GCCCTGCCCAATTTCAAGAGCGCGGCTCT 4817
Oy 464 eluStryThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysL 484
Db 4818 TAGAGAAATGTGTCGCAATGCGAACCACCTTCAGAGAACGATTTAAATTTGATGCA-- 4875
Oy 484 sValIleGluLysGlyTyrArg-----GluLysGlyGlnAl 496
Db 4876 -----ATCGAAGAGCGGCAAAAAATCTTTGAAGAGAGAACTGCTGCAAAAAAGATGTC 4931
Oy 496 aIle-----GluTyrSerGlyLeuThrGluThrG 506
Db 4932 ATTGCTATGAGAGATTAGTGTGCTGAGCTATGATTAATGATGAAGTGCATGACGGA 4991
Oy 506 nLeuArGlnAlaThrGlnLeuAlaIleTyrThrPhe-----ThrAspSe 521
Db 4992 TGGCTATATCGTCATTAACAACCCATTATTTTGTAGTGAAGAATTCAAATGATAA 5051
Oy 521 rAlaGluLeuAspLysAspLysLeuLysAspTyrHisGly-----PheGly----- 536
Db 5052 ACAACCTAGATGAGTGAAGTTGTAAATTATCAACAGACAGAAATGAGGACGTAAGT 5111
Oy 537 -AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSe 556
Db 5112 CAACGAGCAGAGTCAAACCTTAGCGGTGACGATTTTGCAAATTTCAATTCGCGATGACA 5171
Oy 556 rAsnProGlnIleThrAspLeuAspPhePheIleProAsnAsnAsnLysTyrGlnSe 576
Db 5172 GAATAGGCCCAAGGTTACCGATATACATTTCTTGAAATGTCGACGAGAAAGAGTTTCTGA 5231
Oy 576 r----- 576
Db 5232 AATAACACGATAGTACTGGGAAATTTACGCTAAAGGGCTAATGAAGGCATTAGCT 5291
Oy 577 -----LeuIleGlyThrGlnTyrHisProGluAs 586
Db 5292 TTTAGTGAACGAAAGACACACAGGCTATCTGTAGACACACAGCTACATCA----- 5346
Oy 586 PheuValAspIleIleArgMetGlnAspLysGlnValIleProValThrHisAsnIle 606
Db 5347 -----TTTGATGATTAACCGCCCAATTAGGAAAGACAGCAATTCGTTTAGGCGATCTAT 5402
Oy 606 uThrLeuArGlySthrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheG 626
Db 5403 CAATATATCAAGGAAGTCT-----CA 5423

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Oy 626 uIleGluLeuLysAsnAsnLysGlnIleuLeuPheSerGlnThrVal-----LysThrAs 644
Db 5424 ATTAACCAAGAAAGAAAGCAAGACGCTGAACCATTTGACAGTGTGCTTTAAGTATGGA 5483
Oy 644 PLSYThrAsnLeuGlnPheLysAspGlyLysAlaThrIle-----AsnLeuLysHisGlyG 663
Db 5484 TGAACACAGG---CAACCGTAGATGAGCAACCAATCTGATGCTGACAAAGCAAGGCA 5540
Oy 663 uSerLeuThrLeuGlnGlyLeuProGlnGlyTyr----- 674
Db 5541 AGTCATTCGCAAAAACTTAGCACCCGGAACGATGCTTTTGTGAGACACAAGCCCAAC 5600
Oy 675 -SerTyrLeuValLysGlnThrAspSerGlnGlyTyrLys----- 687
Db 5601 TAGCTATCTCTTAATGAAGACGCAAGCGCAAGCTTTAGATTGCCAAAGACCAAGG 5660
Oy 687 ----- 687
Db 5661 CAACACGACCACTGTGCTTAAGCAACCTTTATTAATTAACAAAGTGTGCCAAGCT 5720
Oy 688 -ValLysValAsnSerGlnGlnValAlaAsnAla----- 698
Db 5721 GGTGAATATGATCAGCAAAAGATGCCCTTAGCAGTGTCTGAATTTAAAGTGACAGATGC 5780
Oy 699 -----ThrValSerLysThrGlyIleThrSerAspGlnThrLeuAlaPheG 714
Db 5781 AGAGACAGGCAACACTGTGCTGCTTCATTTAGCTGTGACCAACGAGGTTAGTCAAGT 5840
Oy 714 uAsnAsnLysGlnProValAlaProThrGlyValAspGlnLysIle-----AsnGlyTyr 732
Db 5841 GAACACCTTACACACAGCAAAATATACCTTTTGTGAACAAAGACGCGGATGTTAC 5898

RESULT 15
US-09-071-035-461
; Sequence 461, Application US/09071035
; Patent No. 6448043
; GENERAL INFORMATION:
; APPLICANT: Gill H. Choi
; TITLE OF INVENTION: Enterococcus faecalis polynucleotides and polypeptides
; NUMBER OF SEQUENCES: 496
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,035
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: A. Anders Brookes
; FILING DATE:
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB369P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 461:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

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US-09-071-035-461

## Alignment Scores:

Pred. No.:	5,94e-05	Length:	6168
Score:	149.00	Matches:	181
Percent Similarity:	32.02%	Conservative:	120
Best Local Similarity:	19.26%	Mismatches:	320
Query Match:	3.78%	Indels:	320
		Caps:	45

US-09-494-297-2 (1-757) x US-09-071-035-461 (1-6168)

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OY 19 LeuSerLysAsnSerLysArgPheThValThrLeuValGlyValPheLeuMetIlePhe 38
Db 3361 CTGAGAAACAGCCATGATGAGACGACTATTTTACAGAGCCGCCATTTCCAAATTTGG 3420
OY 39 AlaLeuValThrSerMetVal-----GlyAlaIleLysThr 49
Db 3421 GACCAAGCTAAACACACAGTCTACGTGAAGGTACAGTACAGTCCAGCGGATTATCACA 3480
OY 50 ValPheGly-----LeuValGlySerSerThrProAsnAlaIle 62
Db 3481 TTGTGTGGTGTCCACAAAGGCAATACATTTTGTGGAGACAAAGACCA----- 3531
OY 63 AsnProAspSerSerSerGluTyrArgTrpTyrGlyTyrGluSerTyrValArgGlyHis 82
Db 3532 -----GAGGCTATACAGTTTCGGAC 3552
OY 83 ProTyrTyrLysGlnPheArgValAlaHisAspLeuArgValAsnLeuGluLysSerArg 102
Db 3553 GAATTAGCTTAAGGCCGAGTCATCTACTATTGATGAGAAACTTACGCCGAAGGACACAA 3612
OY 103 SerTyrGlnValTyrCysPheAsnLeuLysAlaPheProLeuGluLysSerAspSerSer 122
Db 3613 CCA---ACCATTTTATAAAGCATGTCATTAAGTATTTTAGAAAAAATGATGAGAGAG 3669
OY 123 ValLysLysTrp-----TyrLysLysHisAspGlyIleSerThrLysPhe--- 137
Db 3670 GGTAAGAAAGTTAGTCAATGCTCGCTTAAATTAGAGCATCCGCTAACACAGCGCTTACT 3729
OY 138 -----GluAspTyrAlaMetSerProArgIleThrGlyLysGluLeuAsnGlnLysLeu 155
Db 3730 CATTTGGAGAAAGTTCCTCCCTTGGCGCCGATCGAAC----- 3765
OY 156 ArgAlaValMetTyrAsnGlnLysProGlnAsnAlaAsnGlyIleMetGlu-----Gly 173
Db 3766 -----AACGCCAATGGCCAGTTAGAGGTGATAGT 3795
OY 174 LeuGluPro---LeuAsnAlaIleArgValThrGlnGluAlaValTrpTyrTyrSerAsp 192
Db 3796 TTAAACCCAGGCTTATCATGTTCCACGAATCGAACGCCAGCGCTATCTTTTAGAC 3855
OY 193 AsnAlaPro----- 195
Db 3856 ACAGACCCCAAGAGTTCATCGTGACACAAATACGAGCGGACCAATTCGTATGTTCA 3915
OY 196 -----IleSerAsnProAspGluSerPheLysArgGluSerGluSerAsn 210
Db 3916 GTCAAAATGCTTAATTACCAAGTTCGTCGAACATAATTAAAAAGCCAAAGCAGCGAAT 3975
OY 211 LeuValSerThrSerGlnLeuSerLeuMet-----ArgGlnAlaLeuLysGln--- 226
Db 3976 CCATTTAGCAGTCTGTAATTTTCAGTCTTGACACACACAGACAGCAAGTTCGAGAAC 4035
OY 227 ---LeuIleAspProAsnLeuAlaThrLysMetProLysGlnValProAspAspPheGln 245
Db 4036 TTAGTTTCGATCCAAACGAAAAAGTCACAGTACGAGATTAGCCCGACGAAAAATATCAA 4095
OY 246 LeuSerIlePheGluSerGluAspLysGlyAspLysTrpLysGlyTyrGlnAsnLeu 265
Db 4096 TTT-----GIGGAACCAAGGCCCA----- 4116
OY 266 LeuSerGlyLysLeuValProThrLysProProThrProGlyAspProPrometProPro 285

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Db 4117 ---GCAGGGTACCTTTTAAACACTGAACCAAGTGTTCACGATTCGACGACGATCGG 4173
OY 286 AsnGlnProGlnThr-----ThrSerVal 293
Db 4174 GGCAAACCCAAACAGTATTAGACAGCGGCTAACTTTGTTACATCATCAGCAGCGCTAAA 4233
OY 294 LeuIleArgLysTyrAlaIleGlyAspTyrSerLysLeuLeuGluAlaThrLeuGln 313
Db 4234 TTATATCAAAAGATGTGATGCA-----CACTATTAGTGTGGACATTTAA 4284
OY 314 LeuThrGlyAspAsnValAsnSerPheGlnAlaIleArgValPheSerSerAsnAspIleGly 333
Db 4285 GTGCTTGATCGAAGGAGAGAAAGATCCAAACAGCGCTTG---ACGACAAATAATCAAGG 4341
OY 334 GluArgGly-----GluLeuSerAspGlyThrTyrThrLeuThrGluLeuAsnSerPro 351
Db 4342 GAATTTGTCACAGACCTTAGCCGCCAGAAATATCGCTTTGTAGAAACCAAGGCCCA 4401
OY 352 AlaGlyTyrSerIle---AlaGluProIleThrPheLysVal-----GluAlaGly 367
Db 4402 ACAGGCTATTATTAAATACACAGCGCAGTCCATTGGAATTCGTGAGAAAAATGCTGGT 4461
OY 368 Lys-----ValTyrThrIle 372
Db 4462 AAACACGCGTGTGTGTCTAGTACAACTTTGTGATTAACAAGGGCTTCCAAATC 4521
OY 373 IleAspGlyLysGlnIleGluAsnPro----- 381
Db 4522 GTGAAAACGATATAGCGGACCAACCATTTAGCAGGCTCTTTTGTGAATATATGATCAC 4581
OY 382 AsnLysGluIleValGluProTyrSerValGluAlaTyrAsnAspPheGluLysPheSer 401
Db 4582 AATAAACA-ATCATTTAGAGTATACAGC-----AACGATGGCAAAAGATGG--- 4625
OY 402 ValLeuThrThrGlnAsnTyr-----AlaLysPhe-TyrTyrAlaLysAs 416
Db 4626 -----CAAAATTTCTTTAGAGACTTGGCGCCGAGTACCTATTATTATTAACAAGA 4673
OY 416 n-----LysAsnGlySerSerGlnValValTyrCys----- 426
Db 4674 AATCAAAAGCACCAAAATTTACCAAGATGGCGAGATTATATTATTTATTCGTAATTAAGAAA 4733
OY 427 ---PheAsnAlaAspLeuLysSerProProAspSerGluAspGlyLysThrMet 444
Db 4734 AGTAAATTCGTGCTGATTTCAAAAGGTATCCGAGATT----- 4773
OY 444 ThrProAspPheThrThrGlyValLysTyrThrHisIleAlaGlyArgAspLeuPhe 464
Db 4774 -----TTCCAATTAGG---GCCCTCGCCAAATTTCAAAAGGACGCCGCTTT 4817
OY 464 eLysTyrThrValLysProArgAspThrAspProAspThrPheLeuLysHisIleLysLys 484
Db 4818 TAAGAAATTTGATGCCAATCGAACCACCTTCCAGAGACGATTTTAAATTGATATGA--- 4875
OY 484 sValIleGluLysGlyTyrArg-----GluLysGlyGlnAl 496
Db 4876 ---ATCGAAACCGGGAATAAATCTTTGAAGAAGAATACGTCGAAATAAGATGGTTC 4931
OY 496 aIle-----GluTyrSerGlyLeuThrGluThrG 506
Db 4932 ATTGGCTATGAGAGATTTAGTGTGTGATGCTATGAAATAGATGAACGTGATCAACGCA 4991
OY 506 nLeuArgAlaAlaThrGlnLeuAlaIleTyrTyrPhe-----ThrAspSe 521
Db 4992 TGGCTATATCGTCAATTAACACCATTTATTTTGTAGTGAGAGAAATTCAAATGATAA 5051
OY 521 rAlaGluLeuAspLysAspLysLeuLysAspTyrHisGly-----PheGly----- 536
Db 5052 ACAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5111
OY 537 AspMetAsnAspSerThrLeuAlaValAlaLysIleLeuValGluTyrAlaGlnAspSe 556

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Db 5112 CAACGACGACGTCACAACTTAGCGGGTGCAGTTTTCGATTTACAAATGCCGATGACA 5171
QY 556 rAsnProGlnLeuThrAspLeuAspPheIleProAsnAsnLysTyrGlnSe 576
Db 5172 GAATCAGCCCCCAAGGTTCCACGATACATCTTGAAATCGTCAGAGAAAAAGTTCTGA 5231
QY 576 r----- 576
Db 5232 AATACACAGCATAGACTGGCGCAATTTACGCTAAAGGCTAAATGAGGCAATTACGT 5291
QY 577 -----LeuIleGlyThrGlnTyrHisProGluAs 586
Db 5292 TTTAGTGAAGAAGCAAGACCAACAGGCTATCTGTAGACACACAGCTACATCCA----- 5346
QY 586 pLeuValAspIleIleArgMetGluAspLysLysGluValIleProValThrHisAsnLe 606
Db 5347 -----TTTGATGTAAACCCGCCCAATTAGGAAAGACAGCAATGCTTTAGCGCATCTTAT 5402
QY 606 uThrLeuArgLysThrValThrGlyLeuAlaGlyAspArgThrLysAspPheHisPheG1 626
Db 5403 CAATTATCAAGAACTGCT-----CA 5423
QY 626 uIleGluLeuLysAsnLysAsnLysGlnGlnLeuLeuSerGlnThrVal-----LysThrAs 644
Db 5424 ATTAAACCAAGAAAGCAAGACAGGTGAAGCATTTGCAAGTGGGTTTAAGTCATTGA 5483
QY 644 pLysThrAsnLeuGluPheLysAspGlyLysAlaThrIle---AsnLeuLysHisGlyG1 663
Db 5484 TGAACACAGGG---CAAAACCGTAGTAGCAAAACCAATCTGATGTGACAAAGCAAGCAA 5540
QY 663 uSerLeuThrLeuGlnGlnLeuProGluGlyTyr----- 674
Db 5541 AGTCATTGCCGAAAACCTTAGCACCGGACAGCATTCGTTTGTGTGAGACACAGCCCAAC 5600
QY 675 -SerTyrLeuValLysGluThrAspSerGluGlyTyrLys----- 687
Db 5601 TAGCTATCTTCTTATATGAACGCGCAAGCTTACGATTCGCAAGACACACCAAGG 5660
QY 687 ----- 687
Db 5661 CAACACGACACTGTGTACTTAAGCACCTTTTATTATTAATTAACCAAGTGCTGCCAAGCT 5720
QY 688 -ValLysValAsnSerGlnGlnValAlaAsnAla----- 698
Db 5721 GGTGAAAATTGATCAGCAAAAGAAATGCCCTTAGCAGGTGCTGAATTTAAAGTACAGATGC 5780
QY 699 -----ThrValSerLysThrGlyIleThrSerAspGluThrLeuAlaPheG1 714
Db 5781 AGAGACAGGCGCAAACTGCGTGTGATTAAGCTTGTGACACCAAGGTTAAGTTCAAGT 5840
QY 714 uAsnAsnLysGluProValValProThrGlyValAspGlnLysIle---AsnGlyTyr 732
Db 5841 GAACCACTTACACACGAGAAATATACCTTTGTGAAACAAAGCACCGGATGTTAC 5898
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Search completed: August 19, 2003, 18:23:10  
Job time : 211 secs

